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 ACCESSION AX333655

VERSION AX333655.1 GI:18124374
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horvath, S., Soppet, D.R., and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
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; Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: An-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
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APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
TELEX:
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TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLONE: 1869688
US-08-966-316-10
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GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Goll, Surya K.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
: TITLE OF INVENTION: PROTEIN KINASES
: NUMBER OF SEQUENCES: 8
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CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: US
: ZIP: 94304
:
COMPUTER READABLE FORM:
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: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSQ Version 2.0
: CURRENT APPLICATION DATA:
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: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0150 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-845-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
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: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
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US-08-749-902-4
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us-09-762-258-1.rn

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Listing first 45 summaries

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-4	260.8	14.4	2610	2	US-09-212-771-1	Sequence 1, Appl 1
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21	145.4	8.0	1273	2	US-08-474-379C-25	Sequence 25, Appl 1
22	145.4	8.0	1273	3	US-09-146-249A-25	Sequence 25, Appl 1
23	145.4	8.0	1273	3	US-08-206-188B-25	Sequence 25, Appl 1
24	142.8	7.9	688	4	US-08-998-416-50	Sequence 90, Appl 1
25	130.6	6.7	2557	4	US-08-464-954A-1	Sequence 1, Appl 1
26	122.4	6.7	2204	1	US-08-221-817-12	Sequence 12, Appl 1
27	122.4	6.7	2204	1	US-08-454-439-12	Sequence 12, Appl 1

28	122.4	6.7	2204	5	PCT-US94-10487-12	Sequence 12, Appl
29	122.4	6.7	2248	4	US-08-466-954A-2	Sequence 2, Appl
30	121.8	6.7	2156	1	US-08-313-274-1	Sequence 1, Appl
31	116.4	6.4	5720	4	US-09-442-100-1	Sequence 1, Appl
32	116.4	6.4	1983	1	US-08-221-817-21	Sequence 21, Appl
33	114.4	6.3	1983	1	US-08-453-439-21	Sequence 21, Appl
34	114.4	6.3	1983	5	PCT-US94-10487-21	Sequence 21, Appl
35	108	5.9	1486	4	US-09-509-902A-15	Sequence 6, Appl
36	108	5.9	1961	4	US-09-509-902A-15	Sequence 15, Appl
37	107.8	5.9	1941	3	US-09-082-737-1	Sequence 1, Appl
38	107.8	5.9	2206	1	US-08-221-817-10	Sequence 10, Appl
39	107.8	5.9	2206	1	US-08-454-439-10	Sequence 10, Appl
40	107.8	5.9	2206	5	PCT-US94-10487-10	Sequence 10, Appl
41	107.4	5.9	1890	3	US-09-289-466-1	Sequence 2, Appl
42	107.4	5.9	1891	3	US-09-289-466-2	Sequence 2, Appl
43	106.8	5.6	3155	4	US-09-442-100-7	Sequence 1, Appl
44	105.8	5.6	1929	2	US-09-016-000-10	Sequence 10, Appl
45	104.8	5.8	2698	2	US-08-677-298-1	Sequence 1, Appl

ALIGNMENTS

```

1 RESULT 1
2 US-09-430-564-1
3 Sequence 1, Application US/09430564
4 Patent No. 6372467
5 GENERAL INFORMATION:
6
7 APPLICANT: John Blesi
8
9 APPLICANT: Kay K. Lee-Funman
10
11 APPLICANT: Calvin J. Kuo
12
13 TITLE OF INVENTION: P5456K AND P8556K GENES, PROTEINS,
14 AND DETECTION METHODS
15
16 FILE REFERENCE: 00246/506002
17
18 CURRENT FILING DATE: 1999-10-29
19
20 CURRENT APPLICATION NUMBER: US/09/430,564
21
22 PRIOR APPLICATION NUMBER: 60/106,141
23
24 PRIOR FILING DATE: 1998-10-29 4
25
26 NUMBER OF SEQ ID NOS: 16
27
28 SOFTWARE: FastSeq for Windows Version 4.0
29
30 SEQ ID NO 1
31
32 LENGTH: 1732
33
34 TYPE: DNA
35
36 ORGANISM: Homo sapiens
37
38 US-09-430-564-1

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94.98; Score 1724; DB 4; Length 1732;

Query Match	94.9%	Score 1724	DB 4	Length 1127
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1724; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

QY	89	CCACGGGCCCCCGGGGCGCGCCCATGCGGCGCGTGTTTGATTGGATTGGAAACG	148
Db	9	CGACGGGCCCGCGGGCCCGCGCCCATGCGCGCGCGTGTTTGATTGGATTGGAAACG	68
QY	149	GAGGAAGCAGCGAGGCGCAGAGGCGAGGCCAGACTCAGCCCGCGGAGCATGTCCCTT	208
Db	69	GAGGAAGCAGCGAGGCGCGAGGCGGAGGCCAGACTCAGCCCGCGGAGCATGTCCCTT	128
QY	209	GCGAGTTGAGGGCAGCTGCGCTAGAGCTGTGGGACACTATGAAGGTGAGCTGACT	268
Db	129	GCGAGTTGAGGGCAGCTGCGCTAGAGCTGTGGGACACTATGAAGAGTGGAGCTGACT	188
QY	269	GAGACCAAGCGTAAAGTTGGCCCAAGAGCGCATGGGCGCCCACTGCGTTGAGTGGTGGGT	328
Db	189	GAGACCAAGCGTAAAGTTGGCCCAAGAGCGCATGGGCGCCCACTGCGTTGAGTGGTGGGT	248
QY	329	GTCCTGGCGCAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAGGTGCAAGGCACCAAC	388
Db	249	GTCCTGGCGCAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAGGTGCAAGGCACCAAC	308
QY	389	TTGGGCAAAATATATCCATGCAATGCTTAAAGAAAGGCCAAAATTGTGGCAATGCCAAG	448
Db	309	TTGGGCAAAATATATCCATGCAATGCTTAAAGAAAGGCCAAAATTGTGGCAATGCCAAG	368

QY	449	GACACGACACACACAGGGCTGTAGCGGAATCTTCTAGAGTACGTGAAGACACCCCTTTATT	508
Db	369	GACACGACACACACAGGGGCTGAGCGGAAATCTTCTAGACGTGAAGACACCCCTTTATT	428
QY	509	GTGGAACCTGGCCATTAGCCTTCCAGACGTGGTGGCAACTCTACCTCATCTCTTGAAGTGCCTC	568
Db	429	GTGGAACCTGGCCATTAGCCTTCCAGACGTGGTGGCAACTCTACCTCATCTCTTGAAGTGCCTC	488
QY	569	ATGTTGGGCGAGCTTCTTACGCATCTGAGCCGAGAGGGGATCTTCTGGAATATAGGGCC	628
Db	489	ATGTTGGGCGAGCTTCTTACGCATCTGAGCCGAGAGGGGATCTTCTGGAATATAGGGCC	548
QY	629	TGCTTCTACCTGGCTGAGATATACGCTGGCCCTGGGCGCATCTCCACTCCAGGGCATATC	688
Db	549	TGCTTCTACCTGGCTGAGATATACGCTGGCCCTGGGCGCATCTCCACTCCAGGGCATATC	608
QY	689	TACCGGGACCTCAAGCCCGAAGCAATCATGCTACAGACCCAGGGCGCAATCAAACTGACG	748
Db	609	TACCGGGACCTCAAGCCCGAAGCAATCATGCTACAGACCCAGGGCGCAATCAAACTGACG	668
QY	749	GACTTTTGACTCTGCAAGGAGTCTATCCATGAGGGCCGCTCACTCAACCTTCTGCGC	808
Db	669	GACTTTTGACTCTGCAAGGAGTCTATCCATGAGGGCCGCTCACTCAACCTTCTGCGC	728
QY	809	ACCAATTGAGTACATGGCCCTGAGATTCTGATGTGCGCAGTGGCGCAACCGGGCTGTGAGC	868
Db	729	ACCAATTGAGTACATGGCCCTGAGATTCTGATGTGCGCAGTGGCGCAACCGGGCTGTGAGC	788
QY	869	TGATGTGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGGATGCGCCCTTTACCGCA	928
Db	789	TGATGTGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGGATGCGCCCTTTACCGCA	848
QY	929	GAGAACCGGAAAGAAACATGTGATTAAGTATCATCGAGGGGCAAGCTGGCAGCTGGCCCTTAC	988
Db	849	GAGAACCGGAAAGAAACATGTGATTAAGTATCATCGAGGGGCAAGCTGGCAGCTGGCCCTTAC	908
QY	989	CTCACCCAGATATGCGCGGGACCTTGTCAAAAAGTTTGTGAACGGATCCAGCCAGCGG	1048
Db	909	CTCACCCAGATATGCGCGGGACCTTGTCAAAAAGTTTGTGAACGGATCCAGCCAGCGG	968
QY	1049	ATTGGGGGTGGCCCAAGGGGATGCTGTGATGTGCGAGAGCAATCCCTTTTCCGGCACAATG	1108
Db	969	ATTGGGGGTGGCCCAAGGGGATGCTGTGATGTGCGAGAGCAATCCCTTTTCCGGCACAATG	1028
QY	1109	AATTGGGAAGACCTTCTGGCTGGCGGTGTGGAGACCCCTTTTCAAGCCCTGTCTCAGTCA	1168
Db	1029	AATTGGGAAGACCTTCTGGCTGGCGGTGTGGAGACCCCTTTTCAAGCCCTGTCTCAGTCA	1088
QY	1169	GAGGAGGACGTBAGCCAGTTTGATATCCCGCTTACACGCGCAACGCGGTGGAGAGTCT	1228
Db	1089	GAGGAGGACGTBAGCCAGTTTGATATCCCGCTTACACGCGCAACGCGGTGGAGAGTCT	1148
QY	1229	GATGACACAGCCCTCAGCGAGAGTGGCAACAGAGCCCTTCTGTGGCTTACATATAGTGGCG	1288
Db	1149	GATGACACAGCCCTCAGCGAGAGTGGCAACAGAGCCCTTCTGTGGCTTACATATAGTGGCG	1208
QY	1289	CCGTCTGTCTGTGACAGACATCAAGGAGGGCTTCTCTTCCAGAGCCAGAGCTGCGCTCACCC	1348
Db	1209	CCGTCTGTCTGTGACAGACATCAAGGAGGGCTTCTCTTCCAGAGCCAGAGCTGCGCTCACCC	1268
QY	1349	AGGGGCGCAAGAGTATGCCCCCGGGGCTCCCGCTCAAGCCCTTCAAGTTCTCCCTTTTGAAG	1408
Db	1269	AGGGGCGCAAGAGTATGCCCCCGGGGCTCCCGCTCAAGCCCTTCAAGTTCTCCCTTTTGAAG	1328
QY	1409	GGGTTTTGGGCCAGGCCACAGCTGTGCGGAGGCGCAAGGAGTACTTACTCTCACACTCTG	1468
Db	1329	GGGTTTTGGGCCAGGCCACAGCTGTGCGGAGGCGCAAGGAGTACTTACTCTCACACTCTG	1388
QY	1469	CCACCCGCGCGCCCTTCGACACACGCGCCCTTCTCCCATCCGCTCCCGCTTCAGAGACCAAG	1528
Db	1389	CCACCCGCGCGCCCTTCGACACACGCGCCCTTCTCCCATCCGCTCCCGCTTCAGAGACCAAG	1448

QY	1529	AAAGTCCAAAGAGGGGCGCTGGGGCGTCCAGGGCCCTAGAAAGCCGGGTGGGGGTGAGGGTAG	1588
Db	1449	AAAGTCCAAAGAGGGGCGCTGGGGCGTCCAGGGCCCTAGAAAGCCGGGTGGGGGTGAGGGTAG	1508
QY	1589	CCCTTGAGCCCTGTCCCTGCGGCGTGTAGAGACAGCAGAACCTTGGGCCAGTTCGCAAGAAC	1648
Db	1509	CCCTTGAGCCCTGTCCCTGCGGCGTGTAGAGACAGCAGAACCTTGGGCCAGTTCGCAAGAAC	1568
QY	1649	CTGGGGGCTGTCTCTGGGGGGTGGGGGTGAGTGGCTGTGAAATGTGTGTCTGTGGGGCA	1708
Db	1569	CTGGGGGCTGTCTCTGGGGGGTGGGGGTGAGTGGCTGTGAAATGTGTGTCTGTGGGGCA	1628
QY	1709	GCTGTCGCCCTCGAATCATGTGGGCACGAGAGGCCGCCGCACACCCCGGCTCAACTGCTC	1768
Db	1629	GCTGTCGCCCTCGAATCATGTGGGCACGAGAGGCCGCCGCACACCCCGGCTCAACTGCTC	1688
QY	1769	CCGTGGAAGATTAAAGGGCTGGAATCATGTGAAAAAAAAAAAAAAAAAAAAA	1812
Db	1689	CCGTGGAAGATTAAAGGGCTGGAATCATGTGAAAAAAAAAAAAAAAAAAAAA	1732

RESULT 2
 US-08-966-316-10
 ; Sequence 10, Application US/08966316
 ; Patent No. 5932445
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Murty, Lynn E.
 ; APPLICANT: Mathur, Preete
 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSO for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/966,316
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ballings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0424 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1637 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: SKINBIT01
 ; CLONE: 18659688
 ; US-08-966-316-10

Query Match 60.88; Score 1104.4; DB 2; Length 1637.
 Best Local Similarity 98.88; Pred. No. 1.2e-248;

1022

us-09-762-258-1.rni

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OY 1175 GAGGTGAGCCAGTTTGATACCCGCTTCACACGGCAGACGCCGAGTCTGTATGAC 1234
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Db 1254 GAGCTGTAG -GAGTTTGATACCCGCTTCACACGGCAGACGCCGAGTCTGTATGAC 1312
OY 1235 ACAGCCCTCAGCGAGTGTGCACACAGGCCCTTCTGGGCTTCACATACGTGGCGCCGTCT 1299
      |||||
Db 1313 ACAG -CTCTACCGGAGATGCCACACAGGCCCTTCTGGGCTT -ACATTAAGTGGCGC -GTCT 1365
OY 1295 GTCCGAGACAG 1305
      |||||
Db 1370 GTCCGTGACAG 1380

RESULT 3
US-08-749-902-4
; Sequence 4, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304

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? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1607 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: Consensus
US-08-749-902-4

Query Match          39.6%; Score 720; DB 2; Length 1607;
Best Local Similarity 99.1%; Pred. No. 5,5e-159;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1.

QY      874  GAGCCTGGGGGCCCTTGATGTGTACGACATGCTACATGATGATCGCGCCCTTTTACCGCAGAGAA 933
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       868  GCGCGCTGGGAGCGCGTGATGTACGACATCTCTACTGTGATCGCGGCCCTTTACCGAGAGAA 927

QY      934  CCGGAGAAACCATGATTAAGATCATCAGGGGCAAGCTGCATCGCCCCCTTAACCTCCAC 993
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       928  CCGGAGAAACCATGATTAAGATCATCAGGGGCAAGCTGCATCTCCCTTACCTCAC 987

QY      994  CCGAGATGCCCGGACCTTGTCAAAAGATTCTGAAACGAGATCCACACGAGGATGG 1053

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Db 988 CCCAGATGCGCCGGACCTTGTCTGCAAAAGTTTCTGAAAGCATCCAGCCGCGATTGG 1047
QY 1054 GGGTGGCCAGGGAGTGTGCTGATGTGCAGACATCCCTTTTCCGGCATGAAATG 1113
Db 1048 GGGTGGCCAGGGAGTGTGCTGATGTGCAGACATCCCTTTTCCGGCATGAAATG 1107
QY 1114 GGACGACCTTCTGGCCCTGTGTGGACCCCTTTTCAGGCCCTGTGTGCAGTACAGGA 1173
Db 1108 GGACGACCTTCTGGCCCTGTGTGGACCCCTTTTCAGGCCCTGTGTGCAGTACAGGA 1167
QY 1174 GGACGTGAGCCAGTTTGTATCCCGCTTTCACAGCCGACACGCGGTGACAGTCTATGA 1233
Db 1168 GGACGTGAGCCAGTTTGTATCCCGCTTTCACAGCCGACACGCGGTGACAGTCTATGA 1227
QY 1234 CACAGCCTTCAGGAGAGTGCACACAGGCCCTTCTGGGCTTCACATAGTGGCCGCTG 1293
Db 1228 CACAGCCTTCAGGAGAGTGCACACAGGCCCTTCTGGGCTTCACATAGTGGCCGCTG 1287
QY 1294 TGTCTGAGACGATCAAGAGAGGCTTCTCTTCACAGCCCAAGCTCGCTCACCCAGCG 1353
Db 1288 TGTCTGAGACGATCAAGAGAGGCTTCTCTTCACAGCCCAAGCTCGCTCACCCAGCG 1347
QY 1354 CTTCAACAGTAGCCCGCGGTCCCGTTCAGCCCGCTCAAGTTCTCCCTTTGAGGGTT 1413
Db 1348 CTTCAACAGTAGCCCGCGGTCCCGTTCAGCCCGCTCAAGTTCTCCCTTTGAGGGTT 1407
QY 1414 TCGGCCAGCCGACGCTGCGGAGCCGACAGGAGTACTACTACCTGCTCCACAC 1473
Db 1408 TCGGCCAGCCGACGCTGCGGAGCCGACAGGAGTACTACTACCTGCTCCACAC 1467
QY 1474 GCGCGCCCTTCAGCACCCGCTCTCCCATCGTCCCGCTTCAGGAGCAGAGAGTC 1533
Db 1468 GCGCGCCCTTCAGCACCCGCTCTCTCCCATCGTCCCGCTTCAGGAGCAGAGAGTC 1527
QY 1534 CAGAGAGGCGCGTGGGCGCTTCAGGAGCCGCTAGGAGACCGGAGTGTAGGCTT 1593
Db 1528 CAGAGAGGCGCGTGGGCGCTTCAGGAGCCGCTAGGAGACCGGAGTGTAGGCTT 1586
QY 1594 GAGCCCTGTCCCTGGCGCTGT 1614
Db 1587 GAGCCCTGTCCCTGGCGCTGT 1607

RESULT 4
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..
US-09-212-771-1

Query Match 14.4%; Score 260.8; DB 2; Length 2610;
Best Local Similarity 56.0%; Pred. No. 8.6e-52;
Matches 562; Conservative 0; Mismatches 427; Indels 15; Gaps 3;

QY 246 ACTATGAAGAGTGAAGCTGACTGAGACCAAGGTTGAGGAGGAGCATCGGGC 305
Db 578 ACAACTCAGGGGCTGAAGAGATGATGTCTCGGCAAGCCCAAGACCGCGTGACCA 637

QY 306 CCCACTGCTTGTAGGTGCTGCGTGTGCTGGCAAGGGGCTTATGCAAGGTGTCCAG 365
Db 638 TGAACGAGTTTATGATCTGAAGCTGTGGGCAAGGCACTTTCGGAAGGTATCC --- 694
QY 366 TGCAGAAAGGTGACAGGACCAACTTGGCAAAATATATGCAATGAAGTCTTAAGGAAG 425
Db 695 -----TGTGAAGAGAGAGGCGCACAGGCGGCTACTACGCCATGMAATCTCTCAAGAGG 748
QY 426 CCAAAATTTGTGCGCAATGCGCAAGAGACACAGCACAGCGGCTGAGCGGACATTTCTAG 485
Db 749 AAGTATGTGTGGCAAGAGAGAGG---TGGCCCAACACTACCGAAGAACCGGCTCTCG 805
QY 486 AGTACGTGAACACCCCTTATTTGTGAAGTGGCTATGCGCTTCCAGCATGGTGGCAAC 545
Db 806 AAGACTCCAGGACACCCCTTCTCTCAACGCCCTGAAGTACTTTCCAGACCCAGAGCGCC 865
QY 546 TCTACCTATCTGATGATGCTCAGTGTGTGGAGAGCTTTCAAGCATCTGAGAGAGAG 605
Db 866 TCTCTTTGTATGAGATGAGCCCAAGCGGGGCGAGCTGTTCACACTGTCCGGGAAC 925
QY 606 GCATCTTCTGTGAAGATACGCGCTGTCTTACTGCTGAGATCAACGCTGCGCTGGCC 665
Db 926 GTGTGTCTCCGAGAGACCGGGCCGCTTCTATGCGCTGAGATGTGTACGCTGAGACT 985
QY 666 ATCTCCACTC---CGAGGCAATCTACCGGGACCTCAAGCCCGAAGAACATCATGCTCA 722
Db 986 AACTGCACTCGGAGAGAAAGAGTGTGTACCGGGACCTCAAGCTGAGAGAACTCATGCTCG 1045
QY 723 GCAGCCAGGGGCGCATCAACAGTACGAGTGTGAGTCTGCAAGAGATCTTATCATAGG 782
Db 1046 ACAAGAGCGGCGCATTAAGATCAGAGACTTGGGCTGTGAAGAGAGGATCAAGACG 1105
QY 783 GCGCCCTCACTCAACCTTCTGCGGCAACATTAAGTATGATGAGCCCTGATGATGTGGTC 842
Db 1106 GTGCCACCATGAAGACCTTTTGGGCAACCTGAGTACTGGCCCCCGAGGTGTGAGG 1165
QY 843 GCAGTGGCCACAAAGGGGCTGTGAGCTGTGAGAGCTGTGGGCGCTTATGATGATGC 902
Db 1166 ACAATGATCTACGGCGCTGTGATGAGAGTGTGGGCTGTGCTATGAGAGATGA 1225
QY 903 TCACTGATGCGCGCTTACCGCAGAGAACCGGAAGAAACATGATGAAGATCATCA 962
Db 1226 TGTGCGGTGCGCTGCTCTTACAAACAGGACCATGAGAGGCTTTTGAAGCTATCTCA 1285
QY 963 GGGGCAAGCTGCACTGCGCCCTTACTCACCCAGATGCCGAGACTTGTCAAAAGT 1022
Db 1286 TGGAGAGATCCGCTTCCCGCGCAGCTTGTGTCGCGGCAAGTCTTGTTCAGGGC 1345
QY 1023 TTTGAAACGGAATCCAGGACGAGGATGGGGTGGCCAGGGGATGCTGTGATGTGC 1082
Db 1346 TGTCAAGAAAGACCCCAAGAGAGGCTTGGCGGGGCTCCGAGGAGCCAAAGAGATCA 1405
QY 1083 AGAAGACATCCCTTTTCCGCAATGAAATTTGGAGCAGCTTGTGGCTGCGCTGTGAGC 1142
Db 1406 TGCAGCATGCTCTTGTTCGCGGTATGCTGTGGCAGACGCTGACGAGAAAGCTCACCC 1465
QY 1143 CCCCTTTCAGGCCCTGCTCTCAGTACAGAGAGAGTACAGTGAAGTTGATACCGCTTCA 1202
Db 1466 CACCTTTCAGGCCCGCAGGTGACGCTCGAGAGACTGACACCGATTTTGTATGAGAGTTCA 1525
QY 1203 CAGGCGCAGCGCGGTGAGCAAGTCTGATGACACAGCCCTCAGC 1246
Db 1526 CGGCCAGATGATCAACATCAACACACCTGACCAAGATGACAGC 1569

RESULT 5
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method

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1  FILE REFERENCE: 4-20683/4/20684/PCt
2
3  CURRENT APPLICATION NUMBER: US/09/091,058
4
5  CURRENT FILING DATE: 1996-06-10
6
7  EARLIER APPLICATION NUMBER: PCT/EP96/04814
8
9  EARLIER FILING DATE: 1996-11-05
10
11 EARLIER APPLICATION NUMBER: 9525703.6
12
13 EARLIER FILING DATE: 1995-12-15
14
15 NUMBER OF SEQ ID NOS: 23
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17 SOFTWARE: PatentIn Ver. 2.0
18
19 SEQ ID NO: 1
20
21 LENGTH: 2610
22
23 TYPE: DNA
24
25 ORGANISM: Homo sapiens
26
27 FEATURE:
28
29 NAME/KEY: CDS
30
31 LOCATION: (199)..(1641)
32
33 US-09-091-058-1

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Query Match	14.4%	Score 260.8;	DB 3	Length 2610;
Best Local Similarity	56.0%	Pred. No. 8.6e-52;		
Matches 562; Conservative	0;	Mismatches 427;		Indels 15; Gaps 3;

Oy	246	ACATTGAAGAGGTGGAGCTGACTGAGACCCAGCTGTACACTTGTGCCCAAGAGGGCATCGGGC	305
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Oy	306	CCCACTGCTTTGAGACTCTGCTGTGCTGTGGGCAAGGGGGGGCTATGAGCAAGGTGTTCCAGG	365
Db	638	TGAAACGACTTTGAGTACCTTAACCTGCTGGGCGCAAGGGCACTTTCGGCAAGGTGATCC---	694
Oy	366	TGCGAAGAGGTGCAGAGCCACCACTTGGGCAAAATATATGCAATGAAAGTCTTAAAGAAAG	425
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Oy	426	CCAAATATTTGGCGCATGTCGCCAAGGACAGACACACAGGGCTAGGCGGAACATTTAG	485
Db	749	AAGTCATCTGGGCGCAAGAGAGAGG---TGCCCCACACATCAACCGAAGAACCGCGCTTGC	805
Oy	486	AGTAGAGAAAGACCCCTTTATTGTGAACATGGCCATGCTTCCAGACTGGTGGCAAC	545
Db	806	AGAACTCCAGGCAACCCCTTCTCACAACCCCTGAAGTACTTTTCCAGACCCACGACGCC	865
Oy	546	TCTACTCATCTTGAATGCTCAGTGTGTGGAGCTCTTCACGATCTGAGCGAGAGG	605
Db	866	TCTGTTGTTCATGAGATGATACGCCACGGGGGCGAGCTGTTCTTCCACCTGTCCGGGAAC	925
Oy	606	GCATCTTCTTGGAAATACGGCCTGCTTCTACTGGCTAAGATCACCTGGCCCTTGGGCC	665
Db	926	GTTGTTTCTCCGAGACCGGGGCCCGTCTATGTGGCCCTGAGATTTGTGTACGGCTGGACT	985
Oy	666	ATTCACACCTC---CCAGGGCATCATGTACCGGGACCTCAAGGCCGGAACATCATGTCACA	722
Db	986	ACCTGCACTGGGAGAAAGACGTGTGTACCGGGACTCAAGCTGGAGAACTCATGTCTGG	1045
Oy	723	GCAGCCAGGGCCACATCAAACTGACCGACTTGTGACTGTGAAGGAGTATATCATGTAGG	782
Db	1046	ACAAGGAGCGGACATTAAGATCAACACTTTCGGGCTGTGCAAGGAGGGGATCAAGGAGC	1105
Oy	783	GGCGCGTACTACACACTTCTGGGGGACCACTTAGTATACATGGCCCCCTAGATTTCTGTGTC	842
Db	1106	GTCGCACCATGAAACACTTTTGTGGGCAACACTAGTACCTTGGCCCCCGCGAGGTGTGGAGG	1165
Oy	843	GCAGTGGGCAACACCGGGCTGTGGACTGTGTGAGAGCTGGGGGGCCCGATGTACGACATGC	902
Db	1166	ACATGTACTACGGCGCTGTGCATGTGACTGTGTGGGGCTGGGCGTGGTCACTATACGAGATGA	1223
Oy	903	TCACTGATTCGCGCCCTTTACGCGAGAGAAACGGAGAAAAACATGATTAAGATCATCA	962
Db	1226	TGTGTGGGTGCGCTCCCTTGTACAAACAGGACCATGAAAGGCTTTTGTAGCTCATCTCA	1285
Oy	963	GGGGCAAGCTGTGGCACTGCCCCCTTACTCTACCCCAATGCTCCGGGACCTTGTCAAAAAGT	1022
Db	1286	TGGAGGAGATCCGCTTCCCGGACAGCTTGTGTGCCAGGCGCAAGTCTTGTCTTTCAGGGC	1345

QY	1023	TTTGAAACGGAATCCAGCAGCAGATTTGGGGTGGCCACGAGATGCTGATATGCG	10822
Db	1346	TGCTCAAGAAAGACCCCAACAGAGCTTTGGCGGGGGCTCGAGAGCGCAAGAGATCA	14058
QY	1083	AGAGACATCCCTTTTCCGGCAGCATGAAATTTGGGAGACACTTTGGCGCTTGGCGTGAGAC	11424
Db	1406	TGCAGCATCGCTTTTTCGGGTAATGCTGTGGCAGCAGCTGTACAGAAAGACCTCAGCC	14555
QY	1143	CCCCCTTAGGCCCTGTCTCAGTCAGAGAGGACGTGAGCCAGTTTGTATACCCGCTTCA	12022
Db	1466	CACCTTCAAGCCCCAGAGTCAAGTCGGAGACTACACAGAGATTTTGTATGAGAGTTCA	15255
QY	1203	CACGGCAGAGCCCGGTGGAAGTCTCTGATGACACAGCCCTCAGC	1246
Db	1526	CGGCGAGATGATCACCATCACACACACCTGACCAAGATCAGACGC	1569

RESULT 6
US-09-256-465-1
; Sequence 1, Application US/09256465

Query Match	14.08;	Score 253.8;	DB 3;	Length 1599;
Best Local Similarity	54.08;	Pred. No. 3.2e-50;		
Matches 569; Conservative	0;	Mismatches 472;	Indels 12;	Gaps 2;

[illegible]

Db	948	CCACATCAAGATCTACCTACTTTGGCCCTGCAAAAGAGGGCATACAGAGAGGGGACCACCAT	1007
Qy	793	TCACACCTTCGCGGCGACCAATTGATGATACATAGGCCCTCGAGATTCGTGTGGAGATGGCGCA	852
Db	1008	GAATAACCTCTGTGTGGAGACCCCGGAGTACCTGTGGCCCTGAGGTGTGGAGCAATGACTA	1067
Qy	853	CAACCGGGCTGTGGACTGTGTGGAGCCCTGGGGGCCCTGATGTACGACATGCTCATCGATTC	912
Db	1068	TGGCGGGGCGGTGACATGTGTGGGGGCTGGGTGTGTGTATGTACGATGATGTGTGGCGCG	1127
Qy	913	GGCGCCCTTTACGCGCAGAGAACCGGAATAATGATTAAGATCATCAGGGGCGACCT	972
Db	1128	CCCTGACCTTCTACAAACGAGGACACGAGCGCCTCTCGAGCTCATCTCATGGAAGAT	1187
Qy	973	GGCAGTGGCCCCCTACCTCAACCCCAATATGCGCGGGACCTGTGCAAAAAGTTCTTAACG	1032
Db	1188	CCGCTTCCCCGGGCACTGCTTCTTCTTCTTCTTCTGCTGTGGCTGTGCTTTAATA	1247
Qy	1033	GAATCCAGCAGCAGCGGATTTGGGGGTGGGCCAGGAGATGTGCTGATGTGTACAGACATCC	1092
Db	1248	GGACCCCAACGACAGGCTTGTGTGGGGGCCCGACGATGCTCAAGAGGTGATGTGAGACAG	1307
Qy	1093	CTTTTCCGGCAGATGAATTTGGAGCAGCCTTCTGGCCGTGGCTGTGTGACCCCTTTTCAG	1152
Db	1308	GTTCCTCTCAGCATCACTGACGAGAGACGTGCTCAGAAAGATCTCTGCCACCTTCA	1367
Qy	1153	GGCCCTGTCTGACGTACAGAGAGGACGTGAGCCAGTTTATACCCGCTTACACGGCAGAC	1212
Db	1368	ACCTCAGGTCACTGCTCCAGGTGTCAACAAGTATCTTGATGTGAATTTACCGGCCACTC	1427
Qy	1213	GCCCGTGGAGATCTCTGATGATACACACCCCTCAGACGAGATGTGCCAACACAGGCCCTTCTGG	1272
Db	1428	CATCAACATCAACCCCCCTGACCGGCTATGACACCCCTGGGCTTACTGTGAGCTGTGACAGC	1487
Qy	1273	CTTACACTACGTGGCGCCGCTGTCTCTGTGGACAGCATCAAGAGGGGCTTCTCTTCCAGCC	1332
Db	1488	GACCACCTTCCCCAGTTTCTCTACTCTGGCGACGATCCGCGAGTGAAGAGTCTGCCACG	1547
Qy	1333	CAAGCTGGGCTCAACCCAGGGGCGCTCAACAGTGA	1365
Db	1548	CAGAGGACGACGCTGCTGCTCCATCCACCGCTGG	1580

RESULT 7
 US-09-167-322-3
 Sequence 3, Application US/09167322
 Patent No. 6365151
 GENERAL INFORMATION:
 APPLICANT: Allgheny University of the Health
 Sciences, Halpern, Michael S.
 England, James M.
 TITLE OF INVENTION: CANCER VACCINE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seidel, Gonda, Lavorina & Monaco, P.C.
 STREET: Suite 1800, Two Penn Center Plaza
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/167,322
 FILING DATE: 07-Oct-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/00582
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:

Query Match	14.0%	Score 253.8	DB 4	Length 1599
Best Local Similarity	54.0%	Pred. No. 3.2e-50		
Matches 569	Conservative 0	Mismatches 477	Indels 12	Gaps 2
NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30.480 REFERENCE/DOCKET NUMBER: 7933-33 PC TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383 TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1599 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-167-322-3				
Query	313	CTTTGAGCTGGCGCTGTGCTGGCGAAGGGGGCTATGGCAAGTGTTCCAGTGGGAAA	372	
Db	540	CTTGACATCATCTCAACATCCTTGGGAAGGAACCTTTGGCAAAAGCATCTGTGGGGGA	599	
Qy	373	GGTGCAGGACCAACTTGGGCAAAATATATGCCATGAATGCTTAAGAGAGCCAAAT	432	
Db	600	G-----AAGGCACATGGCGCGCTACTACCCATGAAGATCTTGCAGGAAGTCAAT	650	
Qy	433	TGTGGCAATGGCAAGGACAGACACACAGAGGGCTGGCGGAACATTCTAGATGCAAT	492	
Db	651	CATTGCCAAGC---ATGAAGTGCCTCACACACTACCGAGACCGGGTCTCTCAGAACAC	707	
Qy	493	GAAGCACCCTTATATGTGGAACCTGGCCATATGCCCTTCCAGACTGGTGGCAACTACCT	552	
Db	708	CAGGACACCGTTCCTCCTACCTGGCGCTGAAGATGCTTCCAGACCCAGACCGCGCTGTCT	767	
Qy	553	CATCTTGAATGCTCCTCAATGATGGGGAGACTCTTCAACGATCTGGAGACGAGAGGCATCT	612	
Db	768	TGTGATGAATGATGCGCAACGGGGGAGACTGTTCTTCAACTGTCTCCGGAGAGCTGTCT	827	
Qy	613	CCTGGAATATAGGCGCTCTTCTACCTGGCTGAGATCAAGCTGGGCCCTGGGCATCTCCA	672	
Db	828	CACAGAGAGAGGGGCGCGGTTTATGATGAGAGAAATGTGCTGGCTCTTGAATCTTGCA	887	
Qy	673	CTTCCAGGSCATCATCTACCGGAGACCTCAAGCCCGAAGCATATGCTCAGACGCAAGG	732	
Db	888	CTGGGGAGCGGTGATACCGGAGATCAAGCTGMAAACTCATGTGGAATAAAGATGG	947	
Qy	733	CCACATCAAACTGACCGACTTGTGACTGTGCAGAGATCTATCCATGAGAGGGCGCGTAC	792	
Db	948	CCACATCAAAATCATGATGACTTTGGCTCTGCAGAAAGGGGACATCATGAGGGCCACCAT	1007	
Qy	793	TCACACTTGTGCGGACCATATGAGTACATGGCCCTGATCTTGTGTGGCGCAGTGGCCA	852	
Db	1008	GAATACTTCTGTGTGGACCCCGGAACTACTGGCGCTTAGGGTGGAGGAAATGACTA	1067	
Qy	853	CACCGGGCTGTGAGCTGTGGAGCTGGGGGCCCTGATGTACGACATGCTACATGATGC	912	
Db	1068	TGGCGGGCCGTGGACTGTGGGGCTGGGTGTGATCATATGAGATGATGTGGCGCG	1127	
Qy	913	GCGGCCCTTACCGGAGAAACCGGAAGAAAAACATGATGAATCATCAGGGGCAACT	972	
Db	1128	CTTGCCCTTCAACAACGAGACACAGACGCGCTTTCAGATCATCTCATGAGAGAT	1187	
Qy	973	GGCACTGGCCCCCTTACCTCACCAGATGCCCGGAGACTTGTCAAAAAGTTTCTAAACG	1032	
Db	1188	CCGCTTCCCGGACAGCGTCAAGCCCGAGGCCAAGTCCCTGTGCTGGCGTGGCTTAAAA	1247	
Qy	1033	GAATCCCAAGCAGGAGATGGGGGGGGCCCAAGGGGATCTGCTGATGTGACAGACATCC	1092	
Db	1248	GGACCCCAAGAGAGGCTTGGTGGGGGGCCCAAGCATGCCAAGAGGATCATGAGACACAG	1307	
Qy	1093	CTTTTCCGGACATGAATTTGGAGACCTTCTGGCGTGGCGTGTGAGACCCCTTTGAG	1152	

Tue Nov 19 10:45:06 2002

us-09-762-258-1.rml

Db 819 ATCTATGAGAAAGATCTCTCTGGAGAGTGGCGCTTCCTCCACTTCAGCTCTGACTTG 878
 Oy 1004 CGGACCTCTGTCAAAAGTTTCTGAAGCAGATCCAGCCAGCGGATGGGGTGGCCCA 1063
 Db 879 AAGGACCTCTGTGGAGACCTCTGAGGTAGATCTCACAGCGCTTTGGGAACTCAAG 938
 Oy 1064 GGGGATGCTGCTGATGTGAGAGATCCCTTTTCCGGGCATGATGATTTGGAGACGCTT 1123
 Db 939 AATGGGGTCAACGATATCAAGAACCAAGTGTGGCACACTGACTGATTTGCCATC 998
 Oy 1124 CTGGCCCTGGCTGGAGCCCTTTTCAGGCCCTGTCTGCAGTCAAGAGAGAGCTGAGC 1183
 Db 999 TACACAGAGAAAGGTGAGAGCTCTTCATATCAAAAGTTTAAAGGCCCTGGGGATACGAGT 1058
 Oy 1184 CAGTTTGA 1191
 Db 1059 AACCTTGA 1066

RESULT 10
 US-08-712-709-6
 ; Sequence 6, Application US/08712709

Patent No. 5863780
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/712,709
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET INFORMATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2311 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; LIBRARY:
 ; CLONE: Consensus
 ; US-08-712-709-6

Query Match 10.9%; Score 198.6; DB: 2; Length 2311;
 Best Local Similarity 53.8%; Pred. No. 2,7e-37;
 Matches 433; Conservative 0; Mismatches 369; Indels 3; Gaps 1;

Oy 399 TATATGCGATGAAGTCTCTAAGAGGCCAAATGTGCGCATGCCAAGAGACAGACAC 458
 Db 377 TCTATGAGTCAAAAGTTTACAGAGAAAGCAATCTGAAAAAGAGAGAGAGACATA 436
 Oy 459 ACAACGGGCTGAGCGGAGACATCTTAGAGTCAGTAGAGACACCCCTTTATGTGAACTGG 518

Db 437 TTATGTCGAGAGCGAATGTCTGTGAAGATGTGAAGAACACCTTCTCTGTCGGCCCTTC 496
 Oy 519 CCTATGCTTCAGAGCTGTGTGGCAAACTCTACTCATCTTGTGAGTGCCTAGTGTGGC 578
 Db 497 ACTTCTCTTCCAGACTGTGTGCAAAATTTGACTTGTCTGACTACTTAATTAATGGTGAG 556
 Oy 579 AGCTCTTCAAGCATCTGAGAGGAGGCGCATCTCTGGAAGATAGCGCTGCTGTATAC 638
 Db 557 AGTGTCTCTCACTCTCCAGAGAGAACGCTGTCTCTGGAACACAGGGCTGCTTCATAG 616
 Oy 639 TGGCTGATACAGCTGAGCCCTTGCCATCTCCACTCCAGAGGCTATCATCCGGAGCC 658
 Db 617 CTGCTGAATTAAGCAAGCTCTGCTGACTGATCTGATCAATCGTTATAGAACT 676
 Oy 699 TCAAGCCGAGACATCATCTGACAGAGGCGCCATCAATCACTGACAGCATTTGGAC 758
 Db 677 TAAACAGAGAAATATTTGCTAGATTCAAGAGGACACATTTCTCTTACTGACTTGGAC 736
 Oy 759 TCTGCAAGAGTCTATCCATGAGGCGCTCTCACTCACACTTCTGCGGACCATTTAGT 818
 Db 737 TCTGCAAGAGAAACATTTGACACAAACAGACACACATCCACCTTGTGCGACCGGAGT 796
 Oy 819 ACATGGCCCTTGAGATCTGTGGTGGCAGTGGCCCAACCGGGCTGTGAGTGTGGAGCC 878
 Db 797 ATCTGCACTGAGGTCTTATAGACAGCCTTATGACAGGACTGTGAGTGTGGTGGC 856
 Oy 879 TGGGGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 916
 Db 857 TGGGAGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 998
 Oy 939 AGAAACCATGATTAAGATCATCAGGGGCAAGCTGAGCAGTCCGCCCTTACCTCAACCCAG 976
 Db 917 CTGAATGTACGACACATCTGACACAGCTCTCAAGTGAACCAAAATTTCAAAAT 976
 Oy 999 ATGCGGAGCTGTGCAAAAGTTTCTGAAGCAGATCCAGCGGAGTGGGGTG 1058
 Db 977 CCGCAAGACACCTCTGAGGGCTCTCTGAGAGGACAGCAAGAGGAGCAAGAGGCTGGG 1033
 Oy 1059 GCCCAGGGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1118
 Db 1034 CCAAGATGACTTCAATGAGATTAAGATGATGATGATGATGATGATGATGATGATG 1093
 Oy 1119 ACCTTGTGCGCTGGGGTGTGAGCCCTTTTCAGGCCCTGTCTGCAAGTCAAGAGAGC 1178
 Db 1094 ATCTATTAATTAAGAAATTAATCTCCCTTTTAAACCAAAATGATGAGGCCCAAGAC 1153
 Oy 1179 TGAAGCAGTTGATACCCGCTTAC 1203
 Db 1154 TAGGCACTTTGACCCCGAGTTTAC 1178

RESULT 11
 US-09-111-444-6
 ; Sequence 6, Application US/09111444
 ; Patent No. 6045792
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5

us-09-762-258-1.rn

Query Match	10.9%	Score 198.6;	DB 3;	Length 2311;
Best Local Similarity	53.8%	Pred. No. 2.7e-37;		
Matches 433; Conservative	0;	Mismatches 369;	Indels 3;	Gaps 1.

[illegible]

RESULT 12

SINEER: 31/7 10000 2100
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.

```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
;

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SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid

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Query Match	10.98;	Score 198.6;	DB 4;	Length 2311;
Best Local Similarity	53.88;	Pred. No. 2.7e-37;	Mismatches 69.	
			Totals 3:	Gaps 1;

[illegible]

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Db 497 ACTTCTCTTCCAGACGCTGACAAATTTGACTTGTCTAGACTACATTAATGATGGAG 556
QY 579 AGCTTCTCAGCATCTGGAGCGAGAGGGCATTTCCGGAAGATAGGCTCTTTTACC 638
Db 557 AGTTGTTCTACATCTCCACAGGAAAGCGTCTCTGGAAACACGGGCTCGTCTTAG 616
QY 639 TGGGTGAGATCACCGCTGGCCCTGGCCCATCTCCACTCCAGGGCATCATACCGGAGC 698
Db 617 CTGCTGAAATAGCCAGTGCCTTGGGCTACCTGATTCATGAAACATGTTATAGAGAT 676
QY 699 TCAAGCCCGAGACATCATCTCAGCAGCAGGCGCACATCAATGACCTTTGGAC 758
Db 677 TAAACAGAGAAATTTTCTGATGATTCACAGGGACACATTTGCTTACTGACTTCGAG 736
QY 759 TCTGCAAGAGTCTATCCATGAGGGCGGCTCCTCAGCCTTTGCGGACCATTTGAGT 818
Db 737 TCTGCAAGGAGAACTTGAACACACAGCAACATCCACCTTCTGTGACCGCGGAGT 796
QY 819 ACATGGCCCTGAGATTCGTGGTGGCAGATGGCCACACCGGCGCTGTGACTGTGAGCC 878
Db 797 ATCTCCGACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGACTGTGTGCTGC 856
QY 879 TGGGGGCGCTGATGTACGACATGCTCATCTGATCGCGCCCTTACCGCAGAGAACCGGA 938
Db 857 TGGGAGCTGTCTGTATGATGATGTGTATGCGCTGCGCTTTTATAGCCGAAACACAG 916
QY 939 AGAAACCATGATTAAGATCATCAGGGGCGAAGCTGCGACCTGCCCCCTACCTACCCAG 998
Db 917 CTGAATGTAGACAAACATTTGAAACAGCCCTCCAGCTGAAACCAATTTACAAATTT 976
QY 999 ATGCCCGGAGCTTGTCAAAAAGTTTGTGAAGAGGAATCCAGCAGGAGATTGGGGGTG 1058
Db 977 CCGCAAGACACTCTCGAGAGGCGCTCTCTGCAAGAGAGACAAAGGGGCTCGGG--G 1033
QY 1059 GCCCAGGGGATCTCTGATGTGACAGACATCCCTTTTCCGGCAGATGAATGGGAGC 1118
Db 1034 CCAAGGATGACTTCAATGAGATTTAGAGTCAATGCTTCTTCTCTTATTAACGGGATG 1093
QY 1119 ACCTTCTGCGCTGGCGTGTGACCCCGCTTTCAGGCCCTGTCTCAGTCAGAGAGAGC 1178
Db 1094 ATCTCATTAATTAAGAAATTTACTCCCTTTTAAACCAAAATGTGATGGGCCCAACGAC 1153
QY 1179 TGAGCCAGTTGATACCGCGCTTAC 1203
Db 1154 TACGGCACTTGTGACCCCGAGTTTAC 1178

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RESULT 13

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US-09-031-295-1
: Sequence 1, Application US/09031295
: Patent No. 6326181
: GENERAL INFORMATION:
: APPLICANT: LANG, Florian
: APPLICANT: WALDEGER, Tullien
: TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: STREET: 3000 K Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/031,295
: FILING DATE: 26-FEB-1998
: CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 197-08-173.8
: FILING DATE: 28-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Sandcock, Colin G.
: REGISTRATION NUMBER: 31,298
: REFERENCE/DOCKET NUMBER: 058315/0123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 672-5300
: TELEFAX: (202) 672-5399
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2370 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 43..1335
: US-09-031-295-1

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Query Match 10.8%; Score 197; DB 4; Length 2370;
 Best Local Similarity 53.7%; Pred. No. 6 4e-37;
 Matches 432; Conservative 0; Mismatches 370; Indels 3; Gaps 1;

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QY 399 TATATGCAATGAATGCTTAAAGAGGCCAAATTTGTGGCAATGCCAAGACAGCAC 458
Db 410 TCTATGCAATGAATGCTTAAAGAGGCCAAATTTGTGGCAATGCCAAGAGGAAAGCA 469
QY 459 ACACAGGGGCGCTGACGGAACATTTAGAGTCAAGTCAAGCAGCCCTTTATGTGCACTGG 518
Db 470 TTTATGCGAGAGCGGAATGTTCTGTGTAAGATGTAAAGACCCCTTCTGCTGCTTTC 529
QY 519 CTTATGCTTCCAGACTGTGCAAACTCTTACCTCATCTGTGAGTCCCTCACTGTGAGCG 578
Db 530 ACTTCTCTTCCAGACTGTGCAAACTCTTACCTCATCTGTGAGTCCCTCACTGTGAGCG 589
QY 579 AGCTTCTCAGCATCTGAGGAGGAGGCGCATCTTCTGGAAGATACGGCTGTCTTACC 638
Db 590 AGTGTGTTACATCTTCCAGAGGAGACGCTGCTTCTGGAACCAAGGCGCTGTCTTATG 649
QY 639 TGGCTGAGATCAAGCTGGCCCTGGCCCATCTTCCATCCAGGCGATCTTACCGGGAGC 698
Db 650 CTGCTGAAATFAGCAGTGCCTTGGGCTACGTCATCTCAATCATCTTATAGAGACT 709
QY 699 TCAAGCCCGAGAAATCATCTCAGCAGCAGGCGCATCAAACTGACGACTTTGGAC 758
Db 710 TAAACACAGAGAAATTTTGTAGATTGACAGGACACATTTGCTTACGATTTCGAGC 769
QY 759 TCTGCAAGAGTCTATCCATGAGGCGCGTCACTCAACACTTCTGGGGACCATTTGAGT 818
Db 770 TCTGCAAGAGAAATTTTGTAGATTGACAGGAGACATCTTCTTGGGACCGCGGAGT 829
QY 819 ACATGCCCCCTGAGATTTGTGTCGCAAGATCCACGCGGCTGTGAGTGTGAGCC 878
Db 830 ATCTGCACTGAGTGTCTTCAATGAGCAGCTTATGACAGAGAGTGTGAGTGTGAGCC 889
QY 879 TGGGGGCGCTGATGAGACATGTCTACTGTGATCGCCGCTTTTACCGCAGAGAACCGGA 938
Db 890 TGGGAGCTGTCTTATGAGTGTCTGATGAGTGTGAGCGCTTCTTATAGCCGAAACAG 949
QY 939 AGAAACCATGATTAATGATCATCGGGGCAAGCTGGGACGCGCCCTTACTACCCACAG 998
Db 950 CTGAATGATGAGCAACATTTCTGAACAGCTCTCCAGCTGAAACCAAAATTTACAAAT 1009
QY 999 ATGCCCGGAGCTTGTCAAAAAGTTTCTGAAGAGATCCACGCGGAGATTTGGGGGTG 1058
Db 1010 CCGCAAGACACTTCTGAGAGGCGCTCTCGAAGAGCAAGGAAAGGCGGCTGGG--G 1066
QY 1059 GCCAGGGAGATGCGTGAATGTGAGAGACATCCCTTTTCCGGCAGATGAATTTGGAGC 1118
Db 1067 CCAAGATGACTTCAATGAGATTAAGATCATGTCTTCTTCTTCAATTAATTAAGTGGAGT 1126

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us-09-762-258-1.rn

QY	309	ACGCGTTAGCGTCGTCGCCGCTGTCCTGGGCAAGGGGGGGCTATGGCCAGAGTGTGTCACAGTTC	368
Db	1110	ACCGATTATTACTTCTCTGTGTGTCTGTGGGAAAGGACGTTTGGCAAGT---CATGCTC	1165
QY	369	GAAAGGTGCAAGGCACCAACTTGTGGGCAAAATATATGCACTGAAGATCTCAAGGAAGGCCA	428
Db	1166	TCAGAGCGGAAGGGGTACA-----GATGMACTATATGCCGTGAAGATCTCGAAGAAGATG	1220
QY	429	AAATGTGGCCAAATGGCCAGAGACACACACACAGCGGCTGAGCGGACATTTCTAGAGT	488
Db	1221	TGTTGATTCAGATGACGATGTGTGAGTCGACACMAATGTGTGGAAGAGAGGTCTGTGGCCCTGC	1280
QY	489	CAGTGAAGCACCCCTTATTTGTGGAATCTGGCCATATGCTTTCACAGACTGTGTGGCAACTCT	548
Db	1281	CTGGGAAGCCCCCATCTCTGTGACTAGCTCCATTCCTCTTCCACAGCATGGAACCGCTCT	1340
QY	549	ACCTCATCCTTGAATGGCTCGATGGTGGGAGCTCTTTCACGCACTCTGGAGCGAGAGGGCA	608
Db	1341	ACTTTGTATGAGATATGTGAACGGGGGGGACACTCATATGTAACCAATCCAAAGTTGGCC	1400
QY	609	TCTTCTGTGAAGATACGGCGCTGCTTACTACGTGGCTGAGATCAAGCTGGGCCCTGGGCCATC	668
Db	1401	GTTTCAAGAGAGCCCATCTGATTTTACGGTCGACAGATTTGCCATCGTCTTTTCTTCT	1460
QY	669	TCCACTCCCAAGGCAATCATACCGGGAGCTCAACCCGAGAACATCATCTGCTCAGACGCC	728
Db	1461	TCCAGAGCAAGGGCACTCATTTTACCGTGTACCTGAACTGAAACCTGAAACGTATGCTGGAATCCG	1520
QY	729	AGGGCCACATCAAACTGACCGCACTTGGACTCTGCAAGAGTCTATCCATGAGGGCGCG	788
Db	1521	AGGGGCAATCAAAATCGCTGACTTGGGATGCTTAAAGAGATATCTGGGATGTGGGGTGA	1588
QY	789	TCACATCAACCTTCCGGGCAACATTGAGTATATGAGCCGCTAGATTTGTGTGTCGCAAGT	848
Db	1581	CAACCAAGACATTTCTGTGCACTCCAGACTACATTTGCCCAAGATCATTTGCTTATACG	1640
QY	849	GCCACAACCGGGCTGTGACTGTGTGAGGCTGTGGGGCCCTGATATACGATGCTACTG	908
Db	1641	CCTAGGGAAGTGTGTGACTGTGTGGGCTTTGGAGTCTCTGTGTATGAAGATGTGGTGGC	1700
QY	909	GATGCGCCGCTTTACCGCAGAGAACCCGGAAGAAAACATGTGATATGATCATCAGGGGCA	968

QY	343	GGGCTATGCGCAGGCTGTTCAGGTGGCAAGATGCAAGCCACCACTTGGGCAAAATTA	402
Db	1123	GGGCAAGGCAAGCTTCGGGAAGGCTGCTTGGAGAGCTGAAAGGCGAGAGGAGTACTC	118
QY	403	TGCGATTGAAGTCTTAAGAGAGGCCAAAATTGTGGCAATTGCCAMGGACACAGCACACAC	462

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Db 1183 TGGCATCAGGCGCTCAGAGAGATGTGTCTGATCGACGACGTGGAGTGCACCAT 1242
OY 463 ACGGGCTGAGCGGAAATTCATAGTCAGTGAACACCCCTTATGTGTGAACGTGCCTA 522
Db 1243 GGTGAGAAAGCGGGTGTGTGACTGTGCCGAGAAATCCCTTCTCACCCACCTCATCTG 1302
OY 523 TGCCTTCCAGACTGTGTGCAACTCTCATCTTGTAGTGCCTCAGTGTGGCGAGCT 582
Db 1303 CACCTTCCAGACCAGGACCCCTGTCTTGTGTGATGAGTTCTCAAGGGGGGAGCT 1362
OY 583 CTTCAGCATCTGTGAGCGAGAGGCGATCTCCGGAAGATACGGCTGCTTACCTGGC 642
Db 1363 GATGTACCATTCAGAGACAAAGCCGCTTGAATCTACGCGTGCACGCTTTATGCCGC 1422
OY 643 TGAATCAGCGTGGCCCTGGGCCATCTCCACTCCAGGCGATCATCTACCGGACCTCA 702
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Search completed: November 18, 2002, 00:30:07
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<p>RESULT 2</p> <p>LOCUS BC000094</p> <p>DEFINITION Homo sapiens, ribosomal protein S6 kinase, 70kD, polypeptide 2, clone MGC:1848 IMAGE:3508140, mRNA, complete cds.</p> <p>ACCESSION BC000094</p> <p>VERSION BC000094.1 GI:12652690</p> <p>KEYWORDS MGC.</p> <p>SOURCE Homo sapiens.</p> <p>ORGANISM Homo sapiens.</p> <p>REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>AUTHORS 1 (bases 1 to 1807)</p> <p>TITLE Strausberg, R.</p> <p>JOURNAL Direct Submission</p> <p>Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</p> <p>REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov</p> <p>COMMENT Contact: MGC help desk</p> <p>Email: cgabs-rt@mail.nih.gov</p> <p>Tissue Procurement: ATCC</p> <p>cDNA Library Preparation: Rubin Laboratory</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Institute for Systems Biology</p> <p>http://www.systemsbiology.org</p> <p>contact: amadamsystemsbiology.org</p> <p>Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan</p>	<p>1807 bp mRNA linear PRI 12-JUN-2001</p>
<p>BASE COUNT 405 a 540 c 545 g 317 t</p>	<p>1662 GATCAAAAGTGTGTCTGTGCTGGGGCACCCTGTGCCCCGATCATGAGGGCAGAGGGCCG 1741</p> <p> </p> <p>1621 GTATGAAGGTGTGTCTGTGCTGGGGCACCCTGTGCCCCGATCATGAGGGCAGAGGGCCG 1680</p> <p> </p> <p>1742 CCCGCGACACCCCGCGGCTCAACTGCTCCCGTGGAGAGATTAAGGAGCTGATCATG 1796</p> <p> </p> <p>1681 CCCGCGACACCCCGCGGCTCAACTGCTCCCGTGGAGAGATTAAGGAGCTGATCATG 1735</p> <p> </p>

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AUTHORS Strausberg,R.			
TITLE Direct Submission			
JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian			
Gene Collection (MGC), Cancer Genomics Office, National Cancer			
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
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Email: ggapbs-remail.nih.gov			
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
CDNA Library Preparation: Rubin Laboratory			
CDNA Sequencing by: The I.M.A.G.E. Consortium (LILU)			
DNA Sequencing by: Genome Sequence Centre,			
BC Cancer Agency, Vancouver, BC, Canada			
info@bcsc.bc.ca			
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,			

Susana Chai, Readman Chiu, Chris Fjell, Erti Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandolf, Anna-Liisa prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 18 Row: a Column: 20
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FEATURES

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QY	386	AACTTGGGCAAAATATATCCCATGAAAGTCTTAAGGAAGGCCAAAATTTGCGCAATGCC	445	
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Db	489	CTCAATGGTGGCGAGCTTTCACCACTGTGGACGAGAGGGCATCTTCTGTGANAATACG	548
QY	626	GCGTCTCTCTACCTGGGTGAGATACACCTGTGGCGGACATGTCCACGCCAGGGCATC	685
Db	549	GCGTCTCTCTACCTGGGTGAGATACACCTGTGGCGGACATGTCCACGCCAGGGCATC	608
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Db	669	ACCGACTTTGGAGCTGTGCAAGAGATCATCATGAGGGCGCGCTCATCAACCTTTGCG	728
QY	806	GGCACCATTTGATGATACATGGCCCTGAGATTCTGGTGGCGAGTGGCCACAAACCGGGCTG	865
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VERSION AF076931.1 GI:5668906
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1716)
AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.
TITLE Characterization of S6K2, a novel kinase homologous to S6K1
JOURNAL Oncogene 18 (36), 5108-5114 (1999)
MEDLINE 99422045
PUBMED 10490847
REFERENCE
2 (bases 1 to 1716)
AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave., Boston, MA 02115, USA
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ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (sites)

AUTHORS

Saitoh,M., ten Dijke,P., Miyazono,K. and Ichijo,H.

TITLE

Cloning and characterization of p70(S6k beta) defines a novel

JOURNAL

Biochem. Biophys. Res. Commun. 253 (2), 470-476 (1998).

MEDLINE

99097259

REFERENCE

2 (bases 1 to 1744)

AUTHORS

Saitoh,M. and Ichijo,H.

TITLE

Direct Submission

JOURNAL

Submitted (27-OCT-1998) Masao Saitoh, Tokyo Medical and Dental Univ., Dept. of Biomaterials Science, Faculty of Dentistry, 1-5-45

Yushima, Bunkyo-ku, Tokyo 113-8549, Japan

(E-mail:msaitoh-indemuln.ac.jp, Tel:+81-3-5603-5473,

Fax:+81-3-5603-0192)

FEATURES

source

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MMU7938

LOCUS MMU7938 1491 bp mRNA Linear ROD 20-NOV-1998

DEFINITION Mus musculus S6 kinase 2.

ACCESSION AJ007938

VERSION AJ007938.1 GI:3901074

KEYWORDS S6 kinase 2; S6K2 gene.

ORGANISM Mus musculus.

Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1491)

Direct Submission

Submitted (15-JUL-1998) Kozma S.C., Growth Control, Friedrich Miescher Institute, P.O. box 2543, Basel, CH-4002, SWITZERLAND

Revised by author

2 (bases 1 to 1491)

Shima, H., Pende, M., Chen, Y., Fumagalli, S., Thomas, G. and Kozma, S.C.

Disruption of the p70(s6k)/p85(s6k) gene reveals a small mouse phenotype and a new functional S6 kinase

EMBO J. 17 (122), 6649-6659 (1998)

99043870

9822608

JOURNAL

PUBMED

FEATURES

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ORIGIN

Query Match 64.0%; Score 1161.6; DB 10; Length 1491;

Best Local Similarity 87.8%; Pred. No. 6.8e-224;

Matches 1282; Conservative 0; Mismatches 169; Indels 9; Gaps 1;

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1 ATGGCGGCGCGTATTTGATTTGATTTGAGACCGGGAAGGAGGAGCGAGGCGAGCA 60

QY	176	CCAGAGCTCAAGCCCCCGGGAGCGATGTCCTCCCTTGGCGAGTTGAGGGACAGTGGCCTAGAG	235
Db	61	CCGAGATTCAACCCCTGGCGAGCGTGTGTCTCTTGGGGAATTAAAGGCTGTGGCCTGGAG	120
QY	236	CCCTGTGGAGCACTGTGAAGAGGTGGAGCTGACTGAGACACAGCGCTCAACGTTGGCCACAG	295
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QY	296	CGCATCGGGCCCCACTGTCTTGAAGCTGTGCGGTGTCTGGCGAAGGGGGCTATGGCAG	355
Db	181	CGCATCGGGCCCCACTGTCTTGAAGCTGACTGAGTGTCTGGCGAAGGGGGGCTATGGCAG	240
QY	356	GTGTTCAGGTGGCAAGGGTGGCAAGGCAACCACTTGGGCAAAAATPATGGCATGGAATC	415
Db	241	GTGTTCAGGTGGCAAAAAGTGGCAAGGCAACCACTTGGGCAAAAATPATGGCATGGAAGTC	300
QY	416	CTAAGGAAGGCGCAAAATTTGTGGCCAAATGGCCAAAGGACACAGCACACAGCGGCTAGCGG	475
Db	301	TTAAGGAAGGCGCAAAATTTGTATGCACTGCCAAGAGACAGCCCATACCCGGGCTAGAGG	360
QY	476	AACATTTCTAGAGTCAGTGAAGCAACCCCTTTATTTGTGAAGCTGGCCTATGCTTCCAGACT	535
Db	361	AACATTTCTAGATCTGTGAAGCATCCCTTCAATTGTATGAACTGGCCTATGCTTCCAGACA	420
QY	536	GGTGGCAAACTCTATCCCTCATCTCGTGGATGCTCAGTGGTGGAGACTCTTCAACACATTT	480
Db	421	GGTGGCAAACTCTATCCCTCATCTCGTGGATGCTCAGTGGTGGAGACTCTTCAACACATTT	480
QY	596	GAGGAGAGGGGCACTCTTCCTGGAAAGATACGGCCCTGTTTACTCTGGCTGAGATCAAGCTG	655
Db	481	GAGGAGAGAGGCACTCTTCTGGAAAGACACAGCTGTTTACTCTGGCAGATTCACACTA	540
QY	656	GCCCTGGGCCATCTCCACTCCCAAGGGCACTATCTACCGGGACCTCAAGCCGAGAACATC	715
Db	541	GCCCTGGGCCATCTCTCAATCCCAAGGCACTATCTACCGGGACCTCAAGGCTGAGAACATC	600
QY	716	ATGCTCAAGCAGCAGGGCCCATCATCAACATCAGACATTTTGAAGCTGTGCAAGAGATCTATC	775
Db	601	ATGCTCAAGCAGCCCGAGGCCCATCAATCAACATCAGATTTTGAAGCTTTCAGAGAGTCCATT	660
QY	776	CATGAGGGGCGCGCATCTCACTCAACCTTCTGGGGACCATTTGAGTACATGGCCCCCTGATAT	835
Db	661	CATGAGGGTGTATCACTTCAACCTTCTGTGGCACCATTGATGATGCCCCAGAGATTT	720
QY	836	CTGTGGCGCAATGCGCAACACCGGGCTGTGTGATGTGTGAGGCTGGGGGCCCTGTGATGAC	895
Db	721	CTAGTGGCGCACTGTGTCAACCGGGCAATGTGTGAGGCTGGAGGCCCTGTGATGAC	780
QY	896	GACATGCTCACTGATGTGCGGCCCTTTACCGCAGAGAACCGGAGAAAACATGTGATTAAG	955
Db	781	GACATGCTCACTGTGATGTGCGGCCCTTCACTGCGAGAACCGGAGAAAACATGTGATTAAG	840
QY	956	ATCATCAAGGGGCAAGCTGGGACATGGCCCCCTCACTCAACCCAGATAGCCCGGACCTGTGC	1015
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QY	1016	AAAAAGTTTCTGAAACGGAATTCACACAGCGGATTTGGGGGTGGGCCACAGGGGATGCTGCT	1075
Db	901	AAAAAGTTTCTGAAAGCGGAACCCCACTCAAGCGAATTTGGGGGTGGGCCAGAGATGTCTGCT	960
QY	1076	GATGTGCAGAGACATCCCTTTTTCGGGCACTGAATTTGGGACGACCTTCTGGCTGGCGCT	1135
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QY	1136	GTGAGACCCCTTTCAGAGCCCTGTGTGCAATGTCAGAGAGAGAGTGAAGCAGTTTATATAC	1195
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QY	1196	CGCTTTCACAGGCGAGAGCGCGGTGGAGCAAGTCTGATGACACAGCCCTCAAGCAGATGTCC	1255
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Db	1141	AAACAAGCCTTCGTGGGGTTACATATATGTGGACCTTCTGTCTCTGTGACAGCATCAAAAG	1200
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Db	1201	GGCTTTCCTTCCAGGCCAAGCTCGTTCTCCAGAGCCCTTAACAGCAGTCCCGCAGC	1260
QY	1376	CCGTCACAGCCCCCAAGTTCTCCCTTTTATGGGGTTTGGGCCAGAGCCCAAGCCTGTGCG	1435
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QY	1436	GAGCCACAGGAGCTACCTCTACCTCAACTCT-----GCCACCGCGCGCGGCTCG	1486
Db	1321	GAGCCCATGGAGCATCTCTACCTCTCAATCTTACCATCACCACCATACCAACCCACA	1380
QY	1487	ACCAACGCCCCCTCTCCCATCCGTCCCGCCCTCAGGAGCAAGAAGTCCAAAGAGGGCGGT	1546
Db	1381	AGCATCGCCCCCTTCCCATCCGTCTCTCCCTCAGGAACCAAGTAAGTCCAAAGAAGGAGCG	1440
QY	1547	GGGGCTCCAGGAGGCTTAGGA	1566
Db	1441	GGCCGCTCAGGGCGTTAGGA	1460

[illegible]

Db	1228	CACAGCCCTCAGGAGAGTGGCCAACCGAGCCCTTCCTCGGGCTTCACATFAGTGGGCGCTT	1287
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Db	1288	TGTCTGTGGACAGCATCAAGAGAGGGCTTCTCTCTTCCAGGCCAAGCTGCGCTACCCAGGCG	1347
QY	1354	CCTCACAGTAGAGCCCCGGGTCCCGCTCAGAGCCCTCAAGTTCTCCCTTTGAGGGGTT	1413
Db	1348	CTCTACAGTAGAGCCCCGGGTCCCGCTCAGAGCCCTCAAGTTCTCCCTTTGAGGGGTT	1407
QY	1414	TGCGCCACGAGCCAGGCTGCGGAGGCCAAGAGCTACTCTCACTCTGCGCAC	1473
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QY	1474	GCGCGCGCCCTGTAGCACAGGCCCCCTTCCCAATCGGTCCCGCTCAGGAGCAAGAATG	1533
Db	1468	GCGCGCGCCCTGTAGCACAGGCCCCCTTCCCAATCGGTCCCGCTCAGGAGCAAGAATG	1527
QY	1534	CAAGAGGGGCGGTGGGCGTCCAGAGGGGCTTAGGAAGCCGGGTGGGGGTGAAGGTAAGCCTT	1593
Db	1528	CAAGAGGGGCGGTGGGCGTCCAGAGGGGCTTAGGAAGCCGGGTGGGGGTGAAGGTAAGCCTT	1586
QY	1594	GAGCCCTGTCCCTGGGCGGT	1614
Db	1587	GAGCCCTGTCCCTGGGCGGT	1607

LOCUS	1800 bp	mRNA	linear	ROD 27-APR-1993
RAT6SKIN3				
DEFINITION	Rat S6 kinase mRNA, complete cds.			
ACCESSION	M57428	M5864		
VERSION	M57428.1	GI:206839		
KEYWORDS	S6 kinase.			
SOURCE	Rat (strain Sprague-Dawley) liver, cDNA to mRNA.			
ORGANISM	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	Kozma,S.C., Ferrari,S., Bassand,P., Slegmann,M., Totty,N. and Thomas,G.			
AUTHORS	1 (bases 1 to 1800)			
TITLE	Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of the second messenger subfamily			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7365-7369 (1990)			
MEDLINE	91017506			
PUBMED	16992226			
REFERENCE	2 (sites)			
AUTHORS	Lane,H.A., Morley,S.J., Doree,M., Kozma,S.C. and Thomas,G.			
TITLE	Identification and early activation of a Xenopus laevis p70s6k following progesterone-induced meiotic maturation			
JOURNAL	EMBO J. 11 (5), 1743-1749 (1992)			
MEDLINE	92256384			
PUBMED	1374712			
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BASE COUNT 556 a 355 c 464 g 425 t
 ORIGIN
 Query Match 34.6%; Score 628.8; DB 10; Length 1800;
 Best Local Similarity 71.1%; Pred. No. 1.2e-116;
 Matches 831; Conservative 0; Mismatches 337; Indels 0; Gaps 0;

QY 240 TGGGACACATATGAGAGGTGAGCTGACTGAGACACAGCTGTAAGCTTGGCCAGAGCGCA 299
 DB 261 TGGAACTTGTGAGAAATTTGAAATCTCAGAACTAGTGAACAGAGGCGCAAAAAA 320
 QY 300 TGGGCCCCACTGCTTTGAGCTGCTGCTGCTGGGCAAGGGGGCTTATGGCAAGTGT 359
 DB 321 TCAGACCCAGATGTTTGTGAGCTACTTGGGCTACTTGGTAAAGGGGCTATGGAAGCTTT 380
 QY 360 TCAGAGTGGCAAGGTCAGACCAACTTGGGCAAAATATATGCGCATGAAGTCTTAA 419
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 DB 741 TTATATCCCAAGTCAAGCTGACAGACTTGGACCTATGCAAGAAATCTTATCATG 800
 QY 780 AGGGCGCCGCTACTCAGACCTTGTGGGCAACATTTGAGTACATGAGCCCTGAGATTCG 839
 DB 801 ATGGACAGTACAGCACCACTTTTGTGGAACAAATAGAAATACATGGCCCTGAAATCTTGA 860
 QY 840 TGGCAGTGGCCACACACCGGGCTGTGAGCTGTGAGACCTTGGGGCCCTGATGACACA 899
 DB 861 TGAAGAACGGGCGCAACACGGCTGTGAGTGTGAGATTTGGGGCAATTAATGATGACACA 920
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 QY 1020 AGTTTTCGAAAGCAATCCACAGCGGATTTGGGGTGGCCCGAGGGGATGCTGCTATG 1079
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 QY 1080 TGCAGAGACATCCCTTTTCCGGACATGAAATTTGGAGACCTTCTGGGCGTGGGCTGG 1139
 DB 1101 TCAGAGCGCATCTCTTTTTCAGACATTAAGTGGGAAGCTTTTGGCTGGGAAGGTGG 1160

QY 1140 ACCCCCTTTCAGGCCCTGTCTGCACTCAGAGAGACAGTGCACCTTTGATACCCGCT 1199
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 QY 1380 TCAGCCCCCTCAAGTCTTCTCCCTTTTGA 1407
 DB 1401 TCAGCCCCAGTCAAAATCTCTCTGGGA 1428

RESULT 11

RATS6PK LOCUS 2287 bp mRNA linear ROD 27-APR-1993
 DEFINITION Rat S6 protein kinase mRNA, complete cds.
 ACCESSION M58340.1 GI:206841
 VERSION 56
 KEYWORDS S6 protein kinase; Insulin/mitogen stimulated protein kinase; p70
 S6 protein kinase.

SOURCE

Rat, cdNA to mRNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

1 (bases 1 to 2287)
 Banerjee,P., Ahmad,M.F., Grove,J.R., Kozlosky,C., Price,D.J. and
 Avruch,J.
 Molecular structure of a major insulin/mitogen-activated 70-kDa S6
 protein kinase
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8550-8554 (1990)
 MEDLINE 91046033
 PUBMED 2236064

FEATURES

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CDS

BASE COUNT 733 a 446 c 540 g 568 t
 ORIGIN
 Query Match 34.6%; Score 628.2; DB 10; Length 2287;
 Best Local Similarity 67.9%; Pred. No. 1.6e-116;
 Matches 892; Conservative 0; Mismatches 418; Indels 3; Gaps 1;

QY 98 CGGGGGCGGCGCGCGCATAGCGCGCGCTTTGATTTGATTTGAGAGAGAGAGAGC 157
 DB 1101 TTTTTCAGACATTAAGTGGGAAGCTTTTGGCTGGGAAGGTGG 1160

Db 224 TGGACATGTGTGAAATTTGAAATCTCAGAACTAGTGTGACAGAGGGCCAGAAAAA 283
QY 300 TCGGGCCCCACTGCTTTGAGCTGCTGCTGCTGGGCAAGGGGGCTATGGCAAGGTGT 359
Db 284 TCAGACCAGATGTTTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343
QY 360 TCCAGGTGCGCAAGAGTGCAGAGGCACTTGGGCAAAATATATGCTATGAAAGTCTAA 419
Db 344 TTCAAGTACGGAAGAAATGACAGGAGCAAAATCTGGGAAAAATTTGCTATGAAAGTCTTA 403
QY 420 GGAAGCCCAAAATTTGTCGCAATGCCAAGGACACAGCAGACAGGCGGTGAGCGAACA 479
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DEFINITION M60725.1 GI:189509
ACCESSION p70 ribosomal S6 kinase alpha-II.
VERSION 60725.1 GI:189509
KEYWORDS Human liver hepatoma, cDNA to mRNA.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1791)
AUTHORS Grove,J.R., Banerjee,P., Balasubramanyam,A., Coffey,P.J., Price,D.J., Avruch,J. and Woodgett,J.R.
TITLE Cloning and expression of two human p70 S6 kinase polypeptides differing only at their amino termini
JOURNAL Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
MEDLINE 92017834
PUBMED 1922062
FEATURES
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Query Match 34.1%; Score 619.8; DB 9; Length 1791;
Best Local Similarity 67.6%; Pred. No. 86-115;
Matches 886; Conservative 0; Mismatches 422; Indels 3; Gaps 1;
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Db 803 ATACATGGCCCTCGAATCTGTATGAGAGTGTGCCAACAATCTGTGTGATGTGTGAG 862
Oy 877 CTTGGGGCCCTGATGTACGACATGCTCACTGATGCGCGCTTACCGCAGAGAACCG 936
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RESULT 14
AX333655
LOCUS AX333655 2346 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4164 from Patent WO0194629.
ACCESSION AX333655

VERSION AX333655.1 GI:18124374
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soper, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 4164 13-DEC-2001;
FEATURES
source location/Qualifiers
1..2346
BASE COUNT 750 a 453 c 558 g 585 t
ORIGIN
Query Match 34.1%; Score 619.8; DB 6; Length 2346;
Best Local Similarity 70.5%; Pred No. 7.8e-115;
Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
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Db 764 ATGGAACAGTCAACACACATTTTGTGGAACATGAAATATGATGATGATGATGATGATG 823
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RESULT 15
HUMP70S6KA 2346 bp mRNA linear PRI 27-ADR-1993
LOCUS Human p70 ribosomal S6 kinase alpha-I mRNA, complete cds.
DEFINITION M60724.1 GI:189507
ACCESSION M60724.1 GI:189507
VERSION p70 ribosomal S6 kinase alpha-I.
KEYWORDS Human liver hepatoma, cDNA to mRNA.
SOURCE Human sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2346)
Grove,J.R., Banerjee,P., Balaubdranyam,A., Coffey,P.J.,
Prlce,D.J., Ayurch,J. and Woodgett,J.R.
Cloning and expression of two human p70 S6 kinase polypeptides
differing only at their amino termini
Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
JOURNAL 92017834
MEDLINE 1922062
PUBMED

FEATURES
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WSLGLMDMLGAPPEPTGENRKTIDKLCKLNPVLTQEBARDLKLKLRNAA
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QAFPMISKREPLRNL"

BASE COUNT 750 a 453 c 358 g 585 t

ORIGIN
Query Match 34.1%; Score 619.8; DB 9; Length 2346;
Best Local Similarity 70.5%; Pred. No. 7.8e-115;
Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
QY 240 TGGGACATATGAAAGGTGGAGCTGACTGACACCGCTGAAAGTTGGCCAGACCGCA 299
Db 224 TGGACATTTGTGAAATTTGAAATCTCAGAAATCTAGTGTGAACACAGAGGCCGAAAAA 283
QY 300 TGGGGCCCACTGCTTTGAGCTGCTGGTGTGGTGGGCAAGGGGGCTATGGCAAGTGT 359
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QY 360 TCCAGGTGGCAAAAGTGTGCAAGGCAACCACTGGGCAAAATATATGCATGAAAGTCTTA 419
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QY 420 GGAAGCCAAATTTGTGCGCAATGCCAAGACACACACACAGCGGCTGAGCGGACA 479
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Db 524 GAAAGCTTACCTCATCTTGAATGCTGAGTGGAGAGAACTATTTATGACTTGAAGT 583
QY 600 GACAGGCACTTCTTGGAAAGATACGCGCTGCTTCTACCTGGCTGAGATCAGCTGGCC 659
Db 584 GAGAGGAAATATTTATGAAAGACACCTGCTTCTTACTTGGGAGAAATCTCCATGGCTT 643
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QY 900 TGCTCACTGATGCGCGCCCTTTACCGCAGAGAACCGAAGAAACCATGATTAAGATCA 959
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Db 1064 TTCAAGCTCATTCATCTTTAGACACATTTAATGGAAGAACTTGTGGCTCGAAAGGTGG 1123
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 00:31:27 ; Search time 2062 Seconds
(without alignments)
14263.338 Million cell updates/sec

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Perfect score: 1816
Sequence: 1 gagagagagagagagagaga.....aaaaaaaaaaaaaaaaaa 1816

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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8: em_hic:*
9: gb_est1:*
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11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	964.4	53.1	992	9	AL529444 AL529444
3	897.6	49.4	1037	14	B0059474 AGENCOURT
4	890.2	49.0	1076	14	BM923000 AGENCOURT
5	868.8	48.8	932	9	AL519475 AL519475
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8 856.8 47.2 1014 14 B0052654 B0052654 AGENCOURT
9 844.2 46.5 849 9 AL527983 AL527983
10 842 46.4 949 14 B0642404 B0642404 AGENCOURT
11 840.4 46.3 895 9 AL521570 AL521570
12 837.4 46.1 907 9 AL563023 AL563023
13 836.2 46.0 952 14 B0918927 B0918927 AGENCOURT
14 827.4 45.6 1075 14 B0062171 B0062171 AGENCOURT
15 806.2 44.4 1048 14 B0052262 B0052262 AGENCOURT
16 802 44.2 1018 14 B0057747 B0057747 AGENCOURT
17 797 43.9 1049 14 B0054269 B0054269 AGENCOURT
18 795.2 43.8 850 9 AL560524 AL560524
19 794.2 43.7 1080 14 B0062488 B0062488 AGENCOURT
20 792.2 43.6 834 12 BE792760 BE792760
21 785 43.2 913 9 AL563439 AL563439
22 778.6 42.9 1176 14 B0061526 B0061526 AGENCOURT
23 776.4 42.8 1044 14 B0072582 B0072582 AGENCOURT
24 773.6 42.6 865 12 BE792968 BE792968 AGENCOURT
25 765.8 42.2 793 13 B1907389 B1907389 AGENCOURT
26 762.4 42.0 764 12 BG773589 BG773589 AGENCOURT
27 762 42.0 789 9 AL525066 AL525066
28 760.6 41.9 854 14 B0431606 B0431606 AGENCOURT
29 755.8 41.6 883 14 B0877063 B0877063 AGENCOURT
30 755.4 41.6 757 13 B1084346 B1084346 AGENCOURT
31 754.8 41.6 867 13 B1821158 B1821158 AGENCOURT
32 754.2 41.5 767 9 AL519476 AL519476
33 753.8 41.5 997 14 B0948653 B0948653 AGENCOURT
34 751.4 41.4 891 12 BG829030 BG829030 AGENCOURT
35 743 40.9 858 14 B0961675 B0961675 AGENCOURT
36 742.4 40.9 923 14 B0890823 B0890823 AGENCOURT
37 739.2 40.7 783 13 B1825778 B1825778 AGENCOURT
38 738.2 40.6 1109 14 B0058742 B0058742 AGENCOURT
39 736.8 40.6 814 12 BG488888 BG488888
40 731.4 40.3 946 9 AL562007 AL562007
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42 719.8 39.6 1082 13 BM561338 BM561338 AGENCOURT
43 711.4 39.2 946 14 B0668937 B0668937 AGENCOURT
44 709.6 39.1 1036 12 BE882270 BE882270
45 707.2 38.9 780 13 B1224008 B1224008

ALIGNMENTS

RESULT 1
AK014412
LOCUS 1834 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830402N06;protein tyrosine phosphatase, receptor type, C polypeptide-associated protein, full insert sequence.
ACCESSION AK014412
VERSION AK014412.1 GI:12852247
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days pregnant adult female placenta and extra embryonic tissue cDNA to mRNA, clone:11b-RIKEN full-length enriched mouse cDNA library clone:3830402N06.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374

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QY	626	GCCCTGCTTACCTGGCTAGATCAGCGTGGCCCTGTGGCAATCTCTACTCTCCAGGGCATC	685
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QY	926	GCANAGAAACGGGAAAGAAACCATATGATTAAGATCATCAGGGGCAACCTGGCACTGCCCCC	985
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Db	541	CCTGGCTGAGATCAACGCTGGGCCCTTGGGCCATCTCCACTTCCAGGGGCATCATCTACCGGGA	600
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Db	601	CCTCAAGCCCGAGAAACATCATCTGCTCAGCAGCCAGGGCCATCAATCAATGACCGACTTTGG	660
QY	757	ACTCTGCAAGAGATCTATCCATGAGGGGGCGCTCACTCAACCTTCTCCGGACCATTTGA	816
Db	661	ACTCTGCAAGAGATCTATCCATGAGGGGGCGCTCACTCAACCTTCTCCGGACCATTTGA	720
QY	817	GTACATGGCCCCCTGAGATTTCTGTGTCGCGAGTGGGCCAACACGGGGCTGTGAGATGTTGAG	876
Db	721	GTACATGGCCCCCTGAGATTTCTGTGTCGCGAGTGGGCCAACACGGGGCTGTGAGATGTTGAG	780
QY	877	CCTGGGGGCCCTGATGTACGACATCTCAGTGATGGCCGCCCTTTACCGCAGAGAACCG	936
Db	781	CCTGGGGGCCCTGATGTACGACATCTCAGTGATGGCCGCCCTTTACCGCAGAGAACCG	840
QY	937	GAAAGAAACCATGTGATTAAGATCATATAGGGGGCAAGTGGGCATGCCCCCTACTACTACCCC	996
Db	841	GAAAGAAACCATGTGATTAAGATCATATAGGGGGCAAGTGGGCATGCCCCCTACTACTACCCC	900
QY	997	AGATGCCCGGGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCACGAGGATTGGGGG	1056
Db	901	AGATGCCCGGGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCACGAGGATTGGGGG	960
QY	1057	TGGCCCAAGGGGATGCTGCTGATGT	1080
Db	961	TGGCCCAAGGGGATGCTGCTGATGT	984
RESULT 3			
LOCUS	BQ059474		
DEFINITION	AGENCOURT 7050085 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815533		
ACCESSION	BQ059474		
VERSION	BQ059474.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1037)		
TITLE	NIH-MGC http://nigc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Lou Staudt cDNA Library Preparation: Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CM2070 row: 0 column: 22 High quality sequence stop: 611. Location/Qualifiers		
FEATURES	1..1037		
SOURCE	/organism="Homo sapiens"		

	BASE COUNT	206 a	356 c	282 g	191 t	2 others
ORIGIN						
Query Match	49.4%;					
Best Local Similarity	95.4%;					
Matches	990;					
Conservative	0;					
Mismatches	36;					
Indels	12;					
Gaps	6;					
Db	612	TCCTGGAGATACGCGCTTCCTTACCTCGCTGAGATACCGCTGGCCCTGGGCACTCC	671			
Db	1	TCCTGGAGATACGCGCTTCCTTACCTCGCTGAGATACCGCTGGCCCTGGGCACTCC	60			
Db	672	ACTCCAGGGCATCTACACGGGAGCTCAAGCCCGAACAATCATCTGCTCAGACAGG	731			
Db	61	ACTCCAGGGCATCTACACGGGAGCTCAAGCCCGAACAATCATCTGCTCAGACAGG	120			
Db	732	GCCACATCAACCTGACCGACTTTGGACTCTGCAGAGTCTATCCATGAGGGCGCTCA	791			
Db	121	GCCACATCAACCTGACCGACTTTGGACTCTGCAGAGTCTATCCATGAGGGCGCTCA	180			
Db	792	CTCACACCTTCTGGGGGACACATTAGTACATAGGCCCCCTGAGATTTGGTGGCGCATGGCC	851			
Db	181	CTCACACCTTCTGGGGGACACATTAGTACATAGGCCCCCTGAGATTTGGTGGCGCATGGCC	240			
Db	852	ACAACCGGGGCTGTGACAGTGAGACCTGGGGGCGCTGATGACAGCATAGCTCATGGAT	911			
Db	241	ACAACCGGGGCTGTGACAGTGAGACCTGGGGGCGCTGATGACAGCATAGCTCATGGAT	300			
Db	912	CGCCGCCCTTACCGCAGAGAAACCGGAAGAAAACCATGGATTAAGTATCAGGGCAAGC	971			
Db	301	CGCCGCCCTTACCGCAGAGAAACCGGAAGAAAACCATGGATTAAGTATCAGGGCAAGC	360			
Db	972	TGGCACTGCCCCCTACCTCAACCCAGATAGCCCGGAGACTTGTCAAAAAGTTTGAAG	1031			
Db	361	TGGCACTGCCCCCTACCTCAACCCAGATAGCCCGGAGACTTGTCAAAAAGTTTGAAG	420			
Db	1032	GGAAATCCAGCAGCGAGGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGCAGACATC	1091			
Db	421	GGAAATCCAGCAGCGAGGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGCAGACATC	480			
Db	1092	CCTTTTTCCGGACATGTAATTGGAGACACTTCTGCGCTGGGCTGTGGACCCCTTTCA	1151			
Db	481	CCTTTTTCCGGACATGTAATTGGAGACACTTCTGCGCTGGGCTGTGGACCCCTTTCA	540			
Db	1152	GGCCCTGTCTGACAGCAGAGGAGAGCAGTGAAGCATTTTGATACCCGCTTACAGCGCAGA	1211			
Db	541	GGCCCTGTCTGACAGCAGAGGAGAGCAGTGAAGCATTTTGATACCCGCTTACAGCGCAGA	600			
Db	1212	CGCCGGTGGACAGTCTCTATGACACAGCCCTTACGAGAGTGTCCCAACGAGGCTTCTGG	1271			
Db	601	CGCCGGTGGACAGTCTCTATGACACAGCCCTTACGAGAGTGTCCCAACGAGGCTTCTGG	660			
Db	1272	GCTTACATATAGTGGCGCGCTGTGTCTGTGGAGACAGCATCAAGAGGGCTTCTCTTCCAGC	1331			
Db	661	GCTTACATATAGTGGCGCGCTGTGTCTGTGGAGACAGCATCAAGAGGGCTTCTCTTCCAGC	720			
Db	1332	CCAACCTGGGCTACACCAAGGCGCTCAACAGTAGAGCCCGGGTTCGCCGTCAGCCCTTCA	1391			
Db	721	CCAACCTGGGCTACACCAAGGCGCTCAACAGTAGAGCCCGGGTTCGCCGTCAGCCCTTCA	780			

OY	1392	AGTCCTCCCTTTGAGGGGTTTGSGCCACGCCACGCTGCCGAGGCCACGGAGCTAC	1451
Db	781	AGTTCTCCCTTTGAGGGGTTTGSGCCACGCCACCTCCGGAGGCCACGGAGCTAC	840
OY	1452	CTTACTCTGCATCTCTGCGACCGCGCCGCGCCCTGACCAACCGCCCTTCCCATCGTC	1511
Db	841	CTTCACT -CACTCCTGCGCA -CGGCGCGCTCTGACACACGCCCTCTTCCATCGTC	898
OY	1512	CCCCCTC -AGGAGCCAAACATCCCAAG -GGGGCGCTGGGGGTCCAGGGCCCTTAGAAGC	1569
Db	899	CCCCCTCAAGGAGACCAAGTCCAAAAGGGGGCCGGGGGCTTCAAGGCCCTTAGAAGC	958
OY	1570	CGGGTGGGGGTAGAGGTAG-----CCCTTAGAGCCCTTCCCTGGCGCTGTAGAGC--A	1621
Db	959	CCCTTTTGGGGGGGTAAAGGTTACCCCTTGACACCTGGCCCTGGGGTGTAAACCA	1018
OY	1622	GCAGGACCCCTGGGCTAGT	1639
Db	1019	CCGGAACCTTGGGCTAGT	1036

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1076)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MCC clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12798 row: f column: 23
 High quality sequence stop: 670.

FEATURES

source

1. .1076

BASE COUNT	ORIGIN
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Query Match	49.08;	Score	890.2;	DB	14;	Length	1076;
Best Local Similarity	96.98;	Pred.	No. 2.9e-139;				
Matches 949; Conservative	0;	Mismatches	25;	Indels	5;	Gaps	4;

86 GCGCGACGGGCCCGGGGCCGCCATGGCGCGCGTGTTCATTGGATTGGAG 145

Db	44	GGCCGACGGGCCCGCCGGGGCCGGGCCGCCCGCCATGCGCGCCCTTTGATTGATTTGGATTGGAG	103
QY	146	ACGGAGGAAGGACACGAGGGCGAGGGCGAGCCAGAGCTCAGCCCGCGGACGATGTCC	205
Db	104	ACGGAGGAAGGACACGAGGGCGAGGGCGAGCCAGAGCTCAGCCCGCGGACGATGTCC	163
QY	206	CTTCCCGAGTTGAGAGCGACTGTGGCTTATGAGCCTGTGGGCACTATTAAGAGSTGAGCTG	265
Db	164	CTTCCCGAGTTGAGAGCGACTGTGGCTTATGAGCCTGTGGGCACTATTAAGAGSTGAGCTG	223
QY	266	ACTGAGACCAAGCGAAGCTTTGGCCCGAGAGCGATGGGCGCCCACTGCTTGAAGTGGTG	325
Db	224	ACTGAGACCAAGCGAAGCTTTGGCCCGAGAGCGATGGGCGCCCACTGCTTGAAGTGGTG	283
QY	326	CGTGTGCTGGGCAAGGGGGGCTTATGGCAAGGTGTTCCAGTTCGAAAGSTGCAMGGCAC	385
Db	284	CGTGTGCTGGGCAAGGGGGGCTTATGGCAAGGTGTTCCAGTTCGAAAGSTGCAMGGCAC	343
QY	386	AACTTTGGGCAAAATATATGTGGCATGAAGAAAGTCCTAAGGAAGGCCAAATTTGTGGCAATACC	445
Db	344	AACTTTGGGCAAAATATATGTGGCATGAAGAAAGTCCTAAGGAAGGCCAAATTTGTGGCAATACC	403
QY	446	AAGGACACAGACACACACGCGGTGAGCGGAACATTCTAGAGTCAGTGAAGCACCCCTTT	505
Db	404	AAGGACACAGACACACACGCGGTGAGCGGAACATTCTAGAGTCAGTGAAGCACCCCTTT	463
QY	506	ATTGTGGAACCTGGCCTTATGCTTCCAGAGCTGGTGGGCAAACTTACCCTATCTTTGAGTGC	565
Db	464	ATTGTGGAACCTGGCCTTATGCTTCCAGAGCTGGTGGGCAAACTTACCCTATCTTTGAGTGC	523
QY	566	CTCAGTGGTGCGAGCTCTTACAGCAATCTGGAACGAGAGGAGATCTTCTGGAGATACG	625
Db	524	CTCAGTGGTGCGAGCTCTTACAGCAATCTGGAACGAGAGGAGATCTTCTGGAGATACG	583
QY	626	GCTGTCTTCTACTGCTGTGAGATCAGCGTGGCCCTGGCCATCTCCATCCGAGGGCATC	685
Db	584	GCTGTCTTCTACTGCTGTGAGATCAGCGTGGCCCTGGCCATCTCCATCCGAGGGCATC	643
QY	686	ATTACACGGGACCTCAAGCCCGAAGCAATCATCTCAGACGACGAGGGCCACATCAACTG	745
Db	644	ATTACACGGGACCTCAAGCCCGAAGCAATCATCTCAGACGACGAGGGCCACATCAACTG	703
QY	746	ACCGACTTTGSACTCTGCAGAGAGTCTATCATAGAGGGCGCGTCACCTACACCTTCTGC	805
Db	704	ACCGACTTTGSACTCTGCAGAGAGTCTATCATAGAGGGCGCGTCACCTACACCTTCTGC	763
QY	806	GGCAACATTGAGTGCATGAGGCCCTGAGATTTCTGGTCGGAGTGGGCCACAAACCGGGCTGTG	865
Db	764	GGCAACATTGAGTGCATGAGGCCCTGAGATTTCTGGTCGGAGTGGGCCACAAACCGGGCTGTG	823
QY	866	GACTGTGTGAGACCTGGGGGG--CCCTGATGTACGACATGCTCACTGTGANTGCGCGCCCTTTAC	924
Db	824	GACTGTGTGAGACCTGGGGGGCCCTGATGTACGACATGCTCACTGTGANTGCGCGCCCTTTCA	883
QY	925	CGCAGAGAACCCGGAAAGAAACATGATTAAGATCATCAGGGGCAA--GCTGGACATGCCCC	983
Db	884	CGCAGAGAACCCGGAAAGAAACCTGTGATTAAGATCTCCGGGGCAAGGCTGGGATCGCCCC	943
QY	984	CC--TACCTCACCCCAATATCCCGGGGACTT--GTCAAAAAGTTTCTGAAAAGGATCCCA	1040
Db	944	CCCTACCTCAAAACCCCAATATCCCGGGGACTT--GTCAAAAAGTTTCTGAAAAGGATCCCA	1003
QY	1041	GCACAGCGGATTTGGGGGTGG 1059	
Db	1004	CCCNCGGGGAATTTTGGGGGG 1022	

RESULT 5	AL519475/c				
LOCUS	AL519475	932 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL519475 LTI_NFL004_NBC2	Homo sapiens cDNA	clone CS0DB004YH05 3		
	prime, mRNA sequence.				

ACCESSION AL519475
 VERSION AL519475.1 GI:12782968
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /clone_1lb="LT1_NF1004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email: fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 169 a 283 c 295 g 163 t 22 others
 ORIGIN
 Query Match 48.8%; Score 886.8; DB 9; Length 932;
 Best Local Similarity 96.6%; Pred. No. 1.1e-138;
 Matches 901; Conservative 21; Mismatches 9; Indels 2; Gaps 2;

QY 824 GCCCTGAGATTTCTGGTGCACATGCGGACACACGGGCTGTGGATGTGGAGCTGGGG 883
 Db 931 GCCCTGAGATTTCTGTGCCAGTGCACACACGGGCTGTGAATGTGGAGCTGGGG 873
 QY 884 GCCCTGATGACATGCTCACTGATGCGCCCTTACCCAGAGAACCGAGAA 943
 Db 872 GCCCTGATGTCACATGCTCACTGATGCGGCGGCTGTGGAGAGAGSSGAGAA 813
 QY 944 ACCATGATTAAGTCAATCAGAGGCAAGCTGGCACTGCCCCCTAACCACCCAGATGCC 1003
 Db 812 ACCATTAATTAAGTCAATCAGAGGCAAGCTGGCACTGCCCCCTAACCACCCAGATGSS 753
 QY 1004 CGGAGACCTTGTCAAAAAGTTTGAAGAGGAATCCAGCAGCGGAGTGGGGTGGCCCA 1063
 Db 752 SGGGASSTTGTSAAAAAGTTTGTGAAGAGGAATCCAGCAGCGGAGTGGGGTGGCCCA 693
 QY 1064 GGGGATGCTGCTGATGTGACAGACATCCCTTTTCCGACATGAATTGGAGCACTT 1123
 Db 692 GGGGATGCTGCTGATGTGACAGACATCCCTTTTCCGACATGAATTGGAGCACTT 633
 QY 1124 CTGGCTGGGCTGTGACACCCCTTTCAAGCCCTGTCTGACATGACAGAGCACTGAGC 1183
 Db 632 CTGGCTGGGCTGTGACACCCCTTTCAAGCCCTGTCTGACATGACAGAGCACTGAGC 573
 QY 1184 CAGTTGATACCGGCTTCAACAGGAGAGCGCGGTGGAGACGTCTATGACACAGCCCTC 1243
 Db 572 CAGTTGATACCGGCTTCAACAGGAGAGCGCGGTGGAGACGTCTATGACACAGCCCTC 513
 QY 1244 AGCGAGAGTGCACACAGGCTTCTGGGCTTGCATACATAGTGGCGGCTGTCTGAGAC 1303
 Db 512 AGCGAGAGTGCACACAGGCTTCTGGGCTTGCATACATAGTGGCGGCTGTCTGAGAC 453

QY 1304 AGCATTAAGAGAGGCTTCTTCCTTCCAGGCCCAAGCTGCTCAACCCAGGCGCTCAACACT 1363
 Db 452 AGCATTAAGAGAGGCTTCTTCCTTCCAGGCCCA-STGCGCTACACCAAGGCGCTCAACACT 394
 QY 1364 AGCCCGGCGGCTCCCTTCAGACCCCTTCAAGTTCTCCCTTTTGAGGGGTTTGCGCCAGC 1423
 Db 393 AGCCCGGCGGCTCCCTTCAGACCCCTTCAAGTTCTCCCTTTTGAGGGGTTTGCGCCAGC 334
 QY 1424 CCCAGCTCCCGAGGCCAAGGAGAGTACCTTACCTCACTCCTGCGACCGCGCGGCC 1483
 Db 333 CCCAGCTCCCGAGGCCAAGGAGAGTACCTTACCTCAGCTCCTGCGACCGCGCGGCC 274
 QY 1484 TCGACCAAGCCGCTTCCCTCATCTCCCTCCCTTCAGGAGACCAAGATTCAGAGGGCC 1543
 Db 273 TCGACCAAGCCGCTTCCCTCATCTCCCTCCCTTCAGGAGACCAAGATTCAGAGGGCC 214
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 Db 213 CGTGGGCGTTCAGAGGCGCTAGGAAGCGGGGTGGGGTGAAGGAGCCCTTGAAGCCCTGTC 154
 QY 1604 CCTGCGGCTGTGAGACAGACAGACCCCTGGCCAGTTCCAGAGACCTGGGGGTGTGCTG 1663
 Db 153 CCTGCGGCTGTGAGACAGACAGACCCCTGGCCAGTTCCAGAGACCTGGGGGTGTGCTG 94
 QY 1664 GGGGTGGGTGTGATGCTGCTATGAAGTGTGTCTGTCTGGGGAGACTGTGCCCTGAAAT 1723
 Db 93 GGGGTGGGTGTGATGCTGCTATGAAGTGTGTCTGTCTGGGGAGACTGTGCCCTGAAAT 34
 QY 1724 CATGGGACGAGAGGCGCGCCGACACACCCCGC 1756
 Db 33 CATGGGACGAGAGGCGCGCCGACACACCCCGC 1

RESULT 6
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 DEFINITION AGENCOURT_6403426 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5517186
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 ACCESSION BM423942
 VERSION BM423942.1 GI:18392154
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1005)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bs-r@mail.nih.gov
 Tissue Procurement: DCTP/DMP
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2018 row: P column: 19
 High quality sequence stop: 746.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_image="IMAGE:5517186"
 /clone_1lb="NIH_MGC_41"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,

FEATURES
 source

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library "

Query Match 47.8%; Score 868.4; DB 13; Length 1005;

Best Local Similarity 98.3%; Pred. No. 1.3e-135; Matches 899; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

BASE COUNT 218 a 288 c 320 g 177 t 2 others
ORIGIN

Query Match 47.8%; Score 868.4; DB 13; Length 1005;
Best Local Similarity 98.3%; Pred. No. 1.3e-135;
Matches 899; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

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146 ACGGAGAGAGCGAG 205
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61 ACGGAGAGAGCGAG 120
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206 CTTGCGAGTTGAG 265
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266 ACTGAGACAGCGTGAACGTTGGCCGAGAGCGCATCGGGCCCACTGCTTGAAGCTGTG 325
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181 ACTGAGACAGCGTGAACGTTGGCCGAGAGCGCATCGGGCCCACTGCTTGAAGCTGTG 240
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386 AACTTGGGCAAAAT 445
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301 AACTTGGGCAAAAT 360
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446 AAGGACACAGACACACACAGGGGCTGAGCGGAACATTTAGAGTCAAGAGCAACCCCTTT 505
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361 AAGGACACAGACACACACAGGGGCTGAGCGGAACATTTAGAGTCAAGAGCAACCCCTTT 420
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421 ATTGGGAACATGGGCTATGGCTTCAGAGTTCGAGCAACCTTACCTCATCTTGAGTGC 480
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566 CTTGAGTGGGCGAGCTTTCACGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625
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601 ATCTACCGGGACCTCAACCCCGAGAACTCATCTCAGACAGAGAGAGAGAGAGAGAGAGAG 660
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746 ACGGACTTTGAGCTCTGCAAGAGAGTCTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 805
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661 ACGGACTTTGAGCTCTGCAAGAGAGTCTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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806 GGCACCATTTGAGTACATGAG 865
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721 GGCACCATTTGAGTACATGAG 780
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866 GACTGTGGAGAGCTGGG-GGGCGCTGATGATGACATGCTCATGATGAGAGAGAGAGAGAGAG 924
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781 GACTGTGGAGAGCTGGGCGGCGCTGATGATGACATGCTCATGATGAGAGAGAGAGAGAGAG 840
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RESULT 7
B0643418 943 bp mRNA linear EST 15-JUL-2002
LOCUS
DEFINITION
AGENCOURT_8485261 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305404
5', mRNA sequence.
B0643418
ACCESSION
VERSION
B0643418.1 GI:21767590
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 943)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.lnl.gov>
plate: LCM2527 row: k column: 05
High quality sequence stop: 775.
Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
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/clone="IMAGE:6305404"
/clone_id="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph. Vector: pOTB7. Site 1: XhoI; Site 2:
EcoRI. cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCGAGAG(5). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 200 a 275 c 298 g 169 t 1 others
ORIGIN

Query Match 47.3%; Score 859.6; DB 14; Length 943;

Best Local Similarity 97.7%; Pred. No. 3.9e-134; Matches 893; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

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146 ACGGAGAGAGCGAG 205
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88 ACGGAGAGAGCGAG 147
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206 CTTGCGAGTTGAG 265
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148 CTTGCGAGTTGAG 207
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266 ACTGAGACAGCGTGAACGTTGGCCGAGAGCGCATCGGGCCCACTGCTTGAAGCTGTG 325
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208 ACTGAGACAGCGTGAACGTTGGCCGAGAGCGCATCGGGCCCACTGCTTGAAGCTGTG 267
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326 CGTGTGCTGGGCAAGGGGGCTATGGCAAGGTTCAGAGTTCGAAAGTTCGAAGCGACC 385
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268 CGTGTGCTGGGCAAGGGGGCTATGGCAAGGTTCAGAGTTCGAAAGTTCGAAGCGACC 327

QY 386 AACTGGGCAAAATATATGTCATGAAAGTCTTAAGAGAGCCAAAATGTGGCAATGCC 445
 DB 328 AACTGGGCAAAATATATGTCATGAAAGTCTTAAGAGAGCCAAAATGTGGCAATGCC 387
 QY 446 AAGGACACAGACACACAGGAGGCTGAGCGGAACATTTAGTACAGTGAAGACACCCCTTT 505
 DB 388 AAGGACACAGACACACAGGAGGCTGAGCGGAACATTTAGTACAGTGAAGACACCCCTTT 447
 QY 506 ATTGTGAAGTGGCTATAGCTTTCAGACTGTGGCAAACTACCTCATCTTGTAGATGC 565
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 DB 508 CTCAGAGTGGCGCAAGCTCTTTCAGAGCATCTGGAGGAGGAGGCTTCTTCTGGAAGATAG 567
 QY 626 GCTGTGCTTACCTGCTGATGATCAGCTGGAGGCTGGGCTCATCTCCAGGAGCATC 685
 DB 568 GCTGTGCTTACCTGCTGATGATCAGCTGGAGGCTGGGCTCATCTCCAGGAGCATC 627
 QY 686 ATCTACCGGAGCTCAAGCCGAGAACATCATCTCAGAGGAGGAGGAGGAGGAGGAGGAGG 745
 DB 628 ATCTACCGGAGCTCAAGCCGAGAACATCATCTCAGAGGAGGAGGAGGAGGAGGAGGAGG 687
 QY 746 ACCGACTTTGAGCTCTGCAAGAGTCTATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 805
 DB 688 ACCGACTTTGAGCTCTGCAAGAGTCTATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747
 QY 806 GGCACCATTTGAGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 865
 DB 748 GGCACCATTTGAGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 807
 QY 866 GACTGTGAGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 924
 DB 808 GACTGTGAGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 867
 QY 925 CGGAGAGAACCGGAGAGAACCATGG-ATTAAGTATCAAGGAGGAGGAGGAGGAGGAGGAGG 963
 DB 868 CGGAGAGAACCGGAGAGAACCATGG-ATTAAGTATCAAGGAGGAGGAGGAGGAGGAGGAGG 927
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 DB 928 CCCCCCTTACTCA 941

RESULT 8
 LOCUS BQ052654 1014 bp mRNA linear EST 29-MAR-2002
 DEFINITION AGENCOURT_6871884 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5934028
 5', mRNA sequence.
 ACCESSION BQ052654
 VERSION BQ052654.1 GI:19811994
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1014)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10C2119 row: 1 column: 05
 High quality sequence stop: 703.
 Location/Qualifiers

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 /db_xref="taxon:9606"
 /clone="IMAGE:5934028"
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 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 225 a 312 c 278 g 197 t 2 others
 ORIGIN

Query Match 47.2%; Score 856.8; DB 14; Length 1014;
 Best Local Similarity 98.4%; Pred. No. 1,1e-133;
 Matches 897; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

QY 356 GGTTCAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 414
 DB 1 GTGTTCCAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
 QY 415 CCTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 474
 DB 61 CCTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 QY 475 GAACATTTAGAGTCAAGTGAAGACCCCTTTATTTGGAAGTGGCTTATGCTTCCAGAC 534
 DB 121 GAACATTTAGAGTCAAGTGAAGACCCCTTTATTTGGAAGTGGCTTATGCTTCCAGAC 180
 QY 535 TGGTGGCAAACTTACCTCATCTGATGAGTGGCTTATGGAAGTGGCTTATGGAAGTGGCTTATG 594
 DB 181 TGGTGGCAAACTTACCTCATCTGATGAGTGGCTTATGGAAGTGGCTTATGGAAGTGGCTTATG 240
 QY 595 GAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 654
 DB 241 GAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 655 GGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 714
 DB 301 GGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 QY 715 CATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 774
 DB 361 CATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 QY 775 CCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 834
 DB 421 CCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 QY 835 TCTGTGCGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 894
 DB 481 TCTGTGCGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 QY 895 CGACATGCTCAGTGGATGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 954
 DB 541 CGACATGCTCAGTGGATGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 QY 955 GATCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1014
 DB 601 GATCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 QY 1015 CAAAAAGTTTCTGAAGAGGAATCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1074
 DB 661 CAAAAAGTTTCTGAAGAGGAATCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
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OY	1135	TGTGACCCCTTTTCAGGCCCGTGCATCAGACGAGAAGAGCACTGGATTGATAC	1194
Dd	761	TETGACCCCCCTTTTCAGGCCCGTGCTCAGTCAGAGAAGACGTGAACACTGGATTGATAC	840
OY	1195	CCGCTTCACAGCGACGCCGCT-GCACAGTCCATGATGACAAG-CCCTACAGCAGAGT	1252
Dd	841	CCGCTTTCACAGCGACGAGACC GG TG G A C A G T C C T G A T G A C A C A C C C C T C A C A G A G A G T	900
OY	1253	GCCAAACGAGCC 1264	
Dd	901	GCCAAACGAGC 912	
RESULT_9			
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DEFINITION	AL527983 LTR_NFL003.NBC3 Homo sapiens CDNA clone CSDDC027HY21.5		
ACCESSION	prime, mRNA sequence.		
VERSION	AL527983		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Ll.M.B., Gruber.C.; Jesse,J. and Polayes,D.		
JOURNAL	Full-length cDNA libraries and normalization unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers 1..849 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSDDC027HY21" /clone.lib="LTR_NFL003_NBC3" /sex="male" /issue_type="neuroblastoma cells" /_lab_host="DH10B" /_note="Organ: brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliangellife@tech.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	178 a 242 c 268 g 159 t	2 others	
ORIGIN			
Query Match	46.5%; Score 844.2; DB 9; Length 849;		
Best Local Similarity	99.8%; Pred.No.1.5e-131;		
Matches 843; Conservative	2; Mismatches 0; Indels 0; Gaps 0;		
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Dd	5	GCCCACGCGGCGCGGGCGCGGCCCCCATGCGCGCGTGTGATTTGATTTGGAG	64
OY	146	ACGAGGAAAGGACGAGGAGGCGAGGCGAAGCATACGCCCGCGGACGACATGTCCC	205
Dd	65	ACGAGGAAAGGAGGAGGAGGCGAGGCGAAGCATACGCCCGCGGACGACATGTMC	124
OY	206	CTTGCCGATTTAGGCGCAGTGTGCTTAAGCCTTGAGGACATAATGAAGAGTGAGCTG	265
Dd	125	C TTG C CG AT GT TA G G G C A G CT GC CT TA AG CCT GT G G G A C A C T A N GA MA G AG TG AC GT G	184
OY	266	ACTGACACGACGTGACGTTGGGCCAGAGGCGATCGGGCCCACTCTTTGAGCTGCTG	325

Db	185	ACTGACACGAGGTACAGTGTGCCACAGCGCATCGGGCCCCCACTGCTTTGAGCTGTG	244
QY	326	CGTGTGCTGGGCAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAAGGTGCAAGGCACC	385
Db	245	CGTGTGCTGGGCAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAAGGTGCAAGGCACC	304
QY	386	AACCTTGGGGCAAAATATATATGTCATGAAAGTCTCCAAAGGAAGGCCAAATATTTGTGGCAATGCC	445
Db	305	AACCTTGGGGCAAAATATATATGTCATGAAAGTCTCCAAAGGAAGGCCAAATATTTGTGGCAATGCC	364
QY	446	AAGGACACAGCAGCACACACAGGGCTAGGCGGAACATTTAGAGTCAAGTCAAGCACCCCTTT	505
Db	365	AAGGACACAGCAGCACACACAGGGCTAGGCGGAACATTTAGAGTCAAGTCAAGCACCCCTTT	424
QY	506	ATTGTGGAACCTGGCCCTATGCTCCCTCCAGACCTGGTGGCAAACTCTACCTCATCTTGGAGTGC	565
Db	425	ATTGTGGAACCTGGCCCTATGCTCCCTCCAGACCTGGTGGCAAACTCTACCTCATCTTGGAGTGC	484
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QY	626	GCCTGCTTCTACCTGGCTGAGATCAACGGTGGCCCTGGGGCAATCTCCATCCAGGGCATC	685
Db	545	GCCTGCTTCTACCTGGCTGAGATCAACGGTGGCCCTGGGGCAATCTCCATCCAGGGCATC	604
QY	686	ATCTACCGGGAGCTTCAAGCCCGAGAAATCATGCTCAGCAGGCAAGGGCCAGATCAAACTG	745
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QY	746	ACCGACTTTGGACTCTGCAGAGAGTCTATCCATGAGGGCGCCGTCACTCACACTTTGCG	805
Db	665	ACCGACTTTGGACTCTGCAGAGAGTCTATCCATGAGGGCGCCGTCACTCACACTTTGCG	724
QY	806	GGCACCATTGAGTATGATGCGCCCTGAGATTCGTGGAGCGAGAGGGCCACACCGGGCTGTG	865
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QY	866	GACTGTGTGAGAGCTGGGGCCCTGATGTACAGCATGCTCACTGATGCGCCGCCCTTTTACC	925
Db	785	GACTGTGTGAGAGCTGGGGCCCTGATGTACAGCATGCTCACTGATGCGCCGCCCTTTTACC	844
QY	926	GCAGA 930	
Db	845	GCAGA 849	
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DEFINITION	AGENCOURT_8485437 NIH_MGC_99 Homo sapiens cdna clone IMAGE:6305367		
ACCESSION	BO642404		
VERSION	BO642404.1	GI:21766576	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 949)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Lou Staudt		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		

Plate: LLCM2527 row: 1 column: 16
High quality sequence stop: 726.

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image:6305367"
/clone_id="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph. Vector: pORF7. Site_1: XhoI. Site_2:
EcoRI. cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAAGCA(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
library."

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[illegible]

Query Match	Score	DB	Length
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Matches 871; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY	86	GGCGAGAGGGCCCGCCGGGGGGCGCGCGCCCATGGCCGGCCCTGTGTTGATTGGATTGGAG	145
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QY	146	ACGAGAGGAAGCACCAGAGGGCGAGGGCGAGCCAGAGCTCAAGCCCCCGCGAGCGATGTGCC	205
Db	88	ACGAGAGGAAGCACCAGAGGGGGAGAGGGGAGGCAAGAGCTCAAGCCCCCGCGAGCGATGTGCC	147
QY	206	CTTGCCGAGTTGAGGGGACAGCTGCGGCTTAGAGGCTCTGGGACACTGTAAAGAGTGGAGCTG	265
Db	148	CTTGCCGAGTTGAGGGGACAGCTGCGGCTTAGAGGCTCTGGGACACTGTAAAGAGTGGAGCTG	207
QY	266	ACTGAGACACCGTGAACGTTGGCCCAAGAGCGCATGCGGGCCCCACAGCTCTTTGAGCTGCTG	325
Db	208	ACTGAGACACCGTGAACGTTGGCCCAAGAGCGCATGCGGGCCCCACAGCTCTTTGAGCTGCTG	267
QY	326	CGTGTGCTGGGCGAAGGGGGGCTATGGCAAGGTGTCCAGGTCGCAAGGAGGAGCAAGGCAACC	385
Db	268	CGTGTGCTGGGCGAAGGGGGGCTATGGCAAGGTGTCCAGGTCGCAAGGAGGAGGCAACC	327
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Db	328	AACTTGGGCAAAATATATATGCCATGAAGAGTCCCTAAGGAAGGCGCAAAATTTGTGCGCAATGCC	387
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QY	506	ATTGTGGAACTGGGCACTATGCTTCCTCAAGACTGTGGGCAAACTCTACCTCATCTTGAAGTGC	565
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QY	566	CTCAGTGGTGGCGAGAGCTTTCACGCATCTGGAGCGAGAGGGGCACTCTTCTGGAAATACG	625
Db	508	CTCAGTGGTGGCGAGAGCTTTCACGCATCTGGAGCGAGAGGGGCACTCTTCTGGAAATACG	567
QY	626	GCGTCGCTTCTACGAGGGGAGATACGCTGGCCCTGGGGCCATCTCCACCTCCCAAGGGCATC	685
Db	568	GCGTCGCTTCTACGAGGGGAGATACGCTGGCCCTGGGGCCATCTCCACCTCCCAAGGGCATC	627
QY	686	ATCTACCGGGAACCTCAAGCCCGAGAACATATGCTCTAGCAAGCCCAAGGGCCACATCAAACTG	745
Db	628	ATCTACCGGGAACCTCAAGCCCGAGAACATATGCTCTAGCAAGCCCAAGGGCCACATCAAACTG	687
QY	746	ACCGACCTTTGGACATCTGCAAGAGATCTATCTCATATGAGGGGCGCGTCACTACACACTTCTGC	805
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QY	806	GGACACATTGAGTACATGGCCCTAGATTCTGGGTGCACAGGGCCACAACCGGGCTGTG	865
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QY	866	GACTGTGTGAGCGCTGGGGCCCTGATGTACGACATGCTACATGATGTCG-CCGCCCTTTAC	924
Db	808	GACTGTGTGAGCGCTGGGGCCCTGATGTACGACATGCTACATGATGTCGCGCCGCTTTCAC	867
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RESULT 11	AL521570	LOCUS	DEFINITION
AL521570	895 bp	mRNA	linear
AL521570	LTL_NFL004_NBC2	Homo sapiens CDNA clone CS05B003YE09 5 prime, mRNA sequence.	EST 13-FEB-2001

FEATURES

Source

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/clone_11p="LTI_NFLO04_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: PCWMSPORT 6; 1st strand cDNA
was primed with a NotI-clo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCWMSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies, a division of Invitrogen 9800 Medical
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filangilife@tech.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT	205	236	264	165	25
ORIGIN	a	c	g	t	others

Stch	Score	DB	Length
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Matches 854; Conservative 24; Mismatches 11; Indels 2; Gaps 2;

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Oy	154	AGGCAGCAGAGGCGAGGCGAGCGAGCAAGCTAGGCCCGCGAGCATGTCCCTTGCGGA	213
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Oy	214	GTTGAGGCGACCTGGCCCTAGAGCCCCCTGTGGGACAATATGAGAGGTGGAGCTGACTGAGAC	273
Dd	121	GTTGAGGCGACCTGGCCCTAARAGCTGTRGMAACTATGAGAGAGGTGGAGCTGAMTGAAM	180
Oy	274	CAGCGTGAACGTGTGGCCAGAGCGCAATCGGGCCCCTACTGTTGAGTCGCTGCGTGCT	333

QY 1591 CTTGACCCCTGTCCTCCGCGCTGTGAGACAGACAGACCCCTGGCCAGTTCCAGAGACCT 1650
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Db 9 TGTGCCCCCT 1

RESULT 13
BQ918927 952 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT 8772806 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372043
DEFINITION 5', mRNA sequence.
ACCESSION BQ918927 GI:22333625
VERSION BQ918927
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM2547 row: c column: 20
High quality sequence stop: 648.
Location/Qualifiers
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/organism="Homo sapiens"
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/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 206 a 275 c 293 g 174 t 4 others
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Query Match 46.0%; Score 836.2; DB 14: Length 952;
Best Local Similarity 96.7%; Pred. No. 3.1e-130;
Matches 897; Conservative 0; Mismatches 24; Indels 7; Gaps 4;

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Db 61 CGGAGAGGCGAGCGAGCGGCGAGCGGCGGAGCGGCGGAGCGTCAAGCCCGCGAGCGATGTCC 120
QY 207 TTGCCAGTTGAGGCGAGCTGGCTAGAGCTTGGGACACTGTGAAGAGTGGAGCTGA 266
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Db 121 TTGCCAGTTGAGGCGAGCTGGCTAGAGCTGTGTGGACATATGCAAGGTGGAGCTGA 180
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Db 181 CTTGAGACAGCGTGAACGTTGGCCAGACGCGATCGGGCCCACTGCTTTGAGCTGTGC 240
QY 327 GTGTGCTGGGCAAGGGGGCTATGGCAGAGTGTTCAGGTGGGAAAGGTGCAAGGCACA 386
Db 241 GTGTGCTGGGCAAGGGGGCTATGGCAGAGTGTTCAGGTGGGAAAGGTGCAAGGCACA 300
QY 387 ACTTGGGCAAAATATATGCTATGAAGAGTCTTAAGGAAGGCCAAATATGGCAATGCCA 446
Db 301 ACTTGGGCAAAATATATGCTATGAAGAGTCTTAAGGAAGGCCAAATATGGCAATGCCA 360
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Db 361 AGGACACAGCACACACACGCGGCTGAGCGGAGACATTTAGAGTCAGTGAAGACCCCTTTA 420
QY 507 TTGTGGAAGTGGGCTATGTGCTTCAGAGCTGTGTGGCAACTTACCTCATCTTGAAGTGC 566
Db 421 TTGTGGAAGTGGGCTATGTGCTTCAGAGCTGTGTGGCAACTTACCTCATCTTGAAGTGC 480
QY 567 TCAGTGTGGCGAGCTCTTCAGGCAATCTGAGGAGAGGAGGCATCTTCGGAAGATAGG 626
Db 481 TCAGTGTGGCGAGCTCTTCAGGCAATCTGAGGAGAGGAGGCATCTTCGGAAGATAGG 540
QY 627 CCGCTTTCTACCTGAGCTGATGATCAGCTGGCCCTGGCCATCTCCACTCCAGGCGATCA 686
Db 541 CCGCTTTCTACCTGAGCTGATGATCAGCTGGCCCTGGCCATCTCCACTCCAGGCGATCA 600
QY 687 TCTACCGGAGCTCAAGCCCGAGACATATGCTACGACGAGGCGCCATCAAACTGA 746
Db 601 TCTACCGGAGCTCAAGCCCGAGACATATGCTACGACGAGGCGCCATCAAACTGA 660
QY 747 CCGACTTTGGACTCTCAAGAGATCTATCCATGAGGAGCCCGCTCACTACACTTCTGCG 806
Db 661 CCGACTTTGGACTCTCAAGAGATCTATCCATGAGGAGCCCGCTCACTACACTTCTGCG 720
QY 807 GCACATTGATGATAGTACGCGCCCTGAGATTCGTGTGGCGAGTGCCCAACCGGGCTGTGG 866
Db 721 GCACATTGATGATAGTACGCGCCCTGAGATTCGTGTGGCGAGTGCCCAACCGGGCTGTGG 780
QY 867 ACTGCTGAGAGCTGTG -GGGGCCCTGATGATGACAGATCTCACTGAGATGGCGCCCTTTA -C 924
Db 781 ACTGCTGAGAGCTGTGAGGAGGCGCCCTGATGATGAGATCTCACTGAGATGGCGCCCTTTACC 840
QY 925 CGGAGAGACCGGAGAGAAACCA -TGGATGAGATCATCAGGGGCA -GCTGGCAGTGTG 979
Db 841 CGGAGAGACCGGAGAGAAACCAANTGNAATGATCATCAGGGGCAAGTGGGAGTGGC 900
QY 980 CCCCCCTACCTCACCCAGATGCCCCGGG 1007
Db 901 CCCCCCTACCTCACCCAGATGCCCCGGG 928

RESULT 14
BQ062171 1075 bp mRNA linear EST 02-APR-2002
LOCUS AGENCOURT 6829901 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5923618
DEFINITION 5', mRNA sequence.
ACCESSION BQ062171
VERSION BQ062171 GI:19888767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LNCM2092 row: 9 column: 11
 High quality sequence start: 2
 High quality sequence stop: 730.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:5923618"
 /clone_lib="NIH_MGC_99"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: pOT87; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCCAGG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the Laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

BASE COUNT 236 a 311 c 335 g 193 t
 ORIGIN

Query Match 45.6%; Score 827.4; DB 14; Length 1075;
 Best Local Similarity 98.2%; Pred. No. 8.9e-129;
 Matches 889; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 86 GGCCGACGGCCCGCGGGCGCGCCGCGCATGCGCGCGTGTGATTGATTGGAG 145
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 Db 35 GGCCACACGGCGCGCGGGCGCGCCGCGCATGCGCGCGTGTGATTGATTGGAG 94
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 QY 146 ACGGAGAAAGGACGAGGGGCGAGCGACGAGCTCAGCCCGCGGACCATGTCCC 205
 |||||||
 Db 95 ACGGAGAAAGGACGAGGGGCGAGCGACGAGCTCAGCCCGCGGACCATGTCCC 154
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 QY 206 CTTGGCGAGTTGAGGCGAGCTGGCTAGAGCCTGTGGGACATATGAGAGGTGAGCTG 265
 |||||||
 Db 155 CTTGGCGAGTTGAGGCGAGCTGGCTAGAGCCTGTGGGACATATGAGAGGTGAGCTG 214
 |||||||
 QY 266 ACTGAGACCAAGCGTAACGTTGGGCCAGAGCGCATCGGGCCACTGCTTTAGCTGCTG 325
 |||||||
 Db 215 ACTGAGACCAAGCGTAACGTTGGGCCAGAGCGCATCGGGCCACTGCTTTAGCTGCTG 274
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 QY 326 CGTGGCTGGGCAAGGGGGGCTATGGAAGTGTCCAGGTGCGAAGGTGCAAGGCACC 385
 |||||||
 Db 275 CGTGGCTGGGCAAGGGGGGCTATGGAAGTGTTCAGGTGCGAAGGTGCAAGGCACC 334
 |||||||
 QY 386 AACCTGGGCAAAATATATGCCATGAAAGTCTTAAGAAAGGCCAAATTTGTGCCAATGCC 445
 |||||||
 Db 335 AACCTGGGCAAAATATATGCCATGAAAGTCTTAAGAAAGGCCAAATTTGTGCCAATGCC 394
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 QY 446 AAGGACACAGCACACAGCGGCTAGCGGAAATTTAGATCAGTGAAGCACCCCTTT 505
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 Db 395 AAGGACACAGCACACAGCGGCTAGCGGAAATTTAGATCAGTGAAGCACCCCTTT 454
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 QY 506 ATTGGGAACGTGGCTATGAGCTTCCAGACTGGTGGCAAACTTACTCATCTCTAGATGC 565
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 Db 455 ATTGGGAACGTGGCTATGAGCTTCCAGACTGGTGGCAAACTTACTCATCTCTAGATGC 514
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 QY 566 CTTCACTGTGGGAGAGCTTTACAGCATCTGAGAGGAGGAGGATCTTCTGTGAAGATAGC 625
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 Db 515 CTTCACTGTGGGAGAGCTTTACAGCATCTGAGAGGAGGAGGATCTTCTGTGAAGATAGC 574
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 QY 626 GCCTGCTTCTACTGCTGATGATCAAGCTGGCCCTGGGCCATCTCCATCCAGGGCATC 685
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 Db 575 GCCTGCTTCTACTGCTGATGATCAAGCTGGCCCTGGGCCATCTCCATCCAGGGCATC 634
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QY 686 ATCTACCGGACCTTCAGGCCCGAGAACATCATGTCTACAGCCAGCGGCACATCAACTG 745
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 QY 806 GGCACCATTTAGTATACATGGCCCTTGAGATTCTGTGGCGCCAGTGGCCCAACAC-GGGCTGT 864
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 Db 755 GGCACCATTTAGTATACATGGCCCTTGAGATTCTGTGGCGCCAGTGGCCCAACACGGGGCTGT 814
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 QY 865 GGACTGTG-TGAGAGTGGGGGCGCTGATGTACGACATGCTCACTGATCGCCGCTTT- 922
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 Db 815 GGACTGTGTTGGAGACCTTGCGGGGCGCTGATGTACGACATGCTCACTGATCGCCGCTTTG 874
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 QY 923 ACCGACAGAAACCGGAG-AAAACCATGATTAAGATCATCAAGGG-CAAGCTGGCATGTC 980
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 Db 875 ACCGACAAAAACCGGAGAAAACCTGGATTAAGATCATCCGGGCAACCTGGCATGTCG 934
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 QY 981 CCCCC 985
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 Db 935 CCCCC 939

RESULT 15

B0052262 1048 bp mRNA linear EST 29-MAR-2002
 LOCUS
 DEFINITION
 AGENCOURT_6868346 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933480
 5', mRNA sequence.

ACCESSION
 B0052262
 VERSION
 B0052262.1 GI:19811602
 KEYWORDS
 EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.ncl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9qbs-remail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

<http://image.llnl.gov>

Plate: LNCM2118 row: b column: 09

High quality sequence stop: 652.

Location/Qualifiers

FEATURES

source

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 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood. Vector: pOT87; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCCAGG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC library."

BASE COUNT 259 a 303 c 290 g 195 t 1 others
 ORIGIN

Query Match 44.4%; Score 806.2; DB 14; Length 1048;

Best Local Similarity 95.0%; Pred. No. 3.1e-125;
Matches 876; Conservative 0; Mismatches 39; Indels 7; Gaps 4;

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Db 1 AGAGCCTGTGGGACACTATGAAAGGTTGGAGTGGAGACCAAGCGTGAAGCTTGGCCC 60
OY 292 AGAGCCTGTGGGACCCCACTGCTTTGAGTGTGCGTGTGCTGGCAAGGGGGCTATGG 351
    |||||||
Db 61 AGAGCCTATGGGCCCCACGCTTTGAGTGTGCGTGTGCTGGCAAGGGGGCTATGG 120
OY 352 CAAGGTGTTCCAGGTGCGAAAGTGCAAGGCACCAACTTGGCAAAATATATGCATGAA 411
    |||||||
Db 121 CAAGGTGTTCCAGGTGCGAAAGTGCAAGGCACCAACTTGGCAAAATATATGCATGAA 180
OY 412 AGTCTAAGGAAGCCAAATTTGGCAATGGCAAGGACACACACACAGGGGCTGA 471
    |||||||
Db 181 AGTCTAAGGAAGCCAAATTTGGCAATGGCAAGGACACACACAGGGGCTGA 240
OY 472 GCGGAACATTCTAGAGTCAGTGAAGCACCCCTTATTTGGAAGTGGCTATGCTTCCA 531
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Db 301 GACTGGTGGCAACTTACTCTCATCTTGAAGTCCCTCAGTGTGGGAGCTTTACGCA 360
OY 592 TCTGAGGCGAGAGGGCATCTTCTGGAAGATAGGGCTGCTTACCTGGCTGAGATCAC 651
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Db 361 TCTGAGGCGAGAGGGCATCTTCTGGAAGATAGGGCTGCTTACCTGGCTGAGATCAC 420
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    |||||||
Db 421 GCTGGCCCTTGGGCAATCTCCACTCCAGGGCATCTTACCGGGACCTCAAGCCGAGAA 480
OY 712 CATCATGCTCAGACGCGAGGCGACATCAAACTGACCGACTTTGGACTTGCAGAGATC 771
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Db 481 CATCATGCTCAGACGCGAGGCGACATCAAACTGACCGACTTTGGACTTGCAGAGATC 540
OY 772 TATCCATGAGGGGCGGCTCACTCACACCTTCTGCGGACCATTGAATGACCCCTGA 831
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OY 892 GTACGACATGCTCAGTGGATCGCCGCCCTTACCSCAGAGAACCGGAACCAATGGA 951
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Db 661 GTACGACATGCTCAGTGGATCGCCGCCCTTACCSCAGAGAACCGGAACCAATGGA 720
OY 952 TAAGATCATCAGGGGCAAGCTGACCTGACCCCTTACCCAGATGCCCCGGA - C 1009
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Db 721 TAAGATCATCAGGGGCAAGCTGACCTGACCCCTTACCCAGATGCCCCGGAACC 780
OY 1010 CTTGTCAAAAAGTTTCTGAACCGAAATCCAGGC - AGCGGATTGGGGGTGCCAGGGG 1067
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Db 781 TTTGTCAAAAAGTTTCTGAACCGAAATCCAGCAACGGAATTTGGGGGTGCCAGGGG 840
OY 1068 ATGCTGTGATGTG - CAGAGACATCCCTTTTCCGGCAGATGAA -- TTGGGACGACCTTC 1124
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Db 841 AAGCTGTCTGAAGGCCAACAACATCCCTTTTTCGGGGCATGAATTTGGGAACAACCTTC 900
OY 1125 TTGGCTGGCGTGTGAGCCGCC 1146
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Db 901 GGGCTTGGCGGGGGGAGCCCC 922
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Search completed: November 18, 2002, 12:11:37
Job time : 2094 secs

* . . *

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Oy	1681	CGTATGAAGTGTTGTGTCTGGTGGGCAGCTGTGCCCCGTGAATCATGGGCACGAGGGCC	1740
Db	1681	CGTATGAAGAAGTGTGTCTGGTGGGCAGCTGTGCCCCGTGAATCATGGGCACGAGGGCC	1740
Oy	1741	GCCCGCCACACC CGCGCTCAACTCTCTCCCTGGAAATTTAAAGGCTGAAATCATGAAAA	1800
Db	1741	GCCCGCCACACC CGCGCTCAACTCTCTCCCTGGAAATTTAAAGGCTGAAATCATGAAAA	1800
Oy	1801	AAAAAAAAAAAAAAAA 1816	
Db	1801	AAAAAAAAAAAAAAAA 1816	
 RESULT 2 AAD37031 ID AAD37031 standard; DNA; 1732 BP.			
XX	AAD37031;		
AC			
DT	27-AUG-2002	(first entry)	
XX			
DE	Human p54S6K DNA.		
KW	Human; mammalian kinase; p54S6K; p85S6K; antibody generation; cancer;		
KX	diagnosis; drug identification; cytostatic; enzyme; gene; ds.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	36..1484	
FT		/tag= a	
FT		/product= "Human p54S6k protein"	
XX			
PN	US6372467-B1.		
PD	16-APR-2002.		
XX			
PF	29-OCT-1999;	99US-0430564.	
XX			
PR	29-OCT-1998;	98US-106141P.	
XX			
PA	(HARD) HARVARD COLLEGE.		
XX			
PI	Blenis J, Lee-fruman KK, Kuo CJ;		
XX			
DR	WPI; 2002-424732/45.		
DR	P-PSDB; AAE23306.		
XX			
PT	Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and		
PT	treating cancers -		
XX			
XX	Example 1; Fig 1A; 30pp; English.		
PS			
XX			
CC	The invention relates to mammalian kinases, p54S6K and p85S6K and		
CC	methods for identifying compounds that modulate, or which are modulated		
CC	by p54S6K and p85S6K. The p54S6K and p85S6K kinases may be used as		
CC	antigens to generate antibodies that may be used in immunoassays to		
CC	detect and quantitate the presence of p54S6K and p85S6K kinases in		
CC	samples and therefore be used to diagnose diseases, e.g. cancers. They		
CC	may also be used in assays as drug targets to identify potential drugs		
CC	for the treatment of diseases associated with p54S6K and p85S6K kinase		
CC	expression and activity. The present sequence is human p54S6K DNA.		
XX			
SQ	Sequence 1732 BP; 355 A; 532 C; 532 G; 313 T; 0 other;		
 Query Match 94.9%; Score 1724; DB 24; Length 1732; Best Local Similarity 100.0%; Pred. No. 0; Matches 1724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	89	CGACGGGCCCCGGGGGCGCGCCGCCAATGCGGCCGCTGTGTAATTGGATTGGAGACG	148

[illegible]

Db 470 TGTCTTACCTGCTGAGATCACGCTGGCCCTGGGCCATCTCCATCCCGAGCATCATC 529
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QY 749 GACCTTGGACTCTGCAAGAGAGTCTATCCATAGAGGGCGCCGTCACATCAACCTTCTGCGGC 808
Db 590 GACTTGGACTCTGCAAGAGAGTCAATCATGAGGGCGCCGTCACATCAACCTTCTGCGGC 649
QY 809 ACCATTAGATACATGCCCCCTGAGATTCTGTGCGCAGTGGCCACAAACCGGGCTGTGAC 868
Db 650 ACCATTAGATACATGCCCCCTGAGATTCTGTGCGCAGTGGCCACAAACCGGGCTGTGAC 709
QY 869 TGGAGGAGCCCTGGGGGCCCTGATGACATGCTACATGATGGCGCCCTTACCCGA 928
Db 710 TGGTGGAGCCCTGGGGGCCCTGATGACATGCTACATGATGGCGCCCTTACCCGA 769
QY 929 GAGAACCGGAGAAAGAACCATGATAGATCATCAGGGGCAAGCTGGCAGTCCCTCCCTAC 988
Db 770 GAGAACCGGAGAAAGAACCATGATAGATCATCAGGGGCAAGCTGGCAGTCCCTCCCTAC 829
QY 989 CTCACCCCGATGCCCCGGGACCTTGTCAAAAAGTTTCTGAACGGAATCCAGCCAGCGG 1048
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Db 950 AATTGGGACGACCTTTCGCTGGCGTGTGAGACCCCTTTCAGAGCCCTGCTCTGACATCA 1009
QY 1169 GAGAGAGACGTGAGCCAGTTTGATACCCGCTTCACACGCGACAGCCGGTGGACAGTCT 1228
Db 1010 GAGAGAGACGTGAGCCAGTTTGATACCCGCTTCACACGCGACAGCCGGTGGACAGTCT 1069
QY 1229 GATGACACAGCCCTCAGGAGAGATGCCAACAGAGCCCTTCGCGGCTTACATACCTGGCG 1288
Db 1070 GATGACACAGCCCTCAGGAGAGATGCCAACAGAGCCCTTCGCGGCTTACATACCTGGCG 1129
QY 1289 CCGTCTGCTCTGAGACAGCATCAAGAGAGGCTTCTCTTCAGACCCCAAGCTCGCTCACCC 1348
Db 1130 CCGTCTGCTCTGAGACAGCATCAAGAGAGGCTTCTCTTCAGACCCCAAGCTCGCTCACCC 1189
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Db 1190 AGGCGCCTCAACAGTAGAGCCCCGGGTCCCGTCAAGCCCTCAAGTCTCCCTTTTGA 1249
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QY 1469 CCACCGCGCGCCCTCGACACAGCCCTCTCCCATCCCTCCCTCCAGAGACAAAG 1528
Db 1310 CCACCGCGCGCCCTCGACACAGCCCTCTCCCATCCCTCCCTCCAGAGACAAAG 1369
QY 1529 AAGTCCAAAGAGGGGCGTGGCGTCCAGAGGCGCTAGAGAGCCGGGTGGGGTGAAGGTAG 1588
Db 1370 AAGTCCAAAGAGGGGCGTGGCGTCCAGAGGCGCTAGAGAGCCGGGTGGGGTGAAGGTAG 1429
QY 1589 CCCTTGAGACCTCTGCTCCCTGCGGCTGTGAGACAGAGAGACCCCTGGGCCAGTTTCCAGAAC 1648
Db 1430 CCCTTGAGACCTCTGCTCCCTGCGGCTGTGAGACAGAGAGACCCCTGGGCCAGTTTCCAGAAC 1489
QY 1649 CTGGGGGTGTGTGGGGGTGGGGGTGATGAGTAAAGTGTGTGTCTGCTGGGCA 1708
Db 1490 CTGGGGGTGTGTGGGGGTGGGGGTGATGAGTAAAGTGTGTGTCTGCTGGGCA 1549
QY 1709 GCTGTGCCCTGAAATCATGAGGACGAGAGGCGCCCGCCACACCCCGGCTCAACTGCTC 1768
Db 1550 GCTGTGCCCTGAAATCATGAGGACGAGAGGCGCCCGCCACACCCCGGCTCAACTGCTC 1609

QY 1769 CCGTGAAGATTAAAGGCTGAATCATGAAAAA 1806
Db 1610 CCGTGAAGATTAAAGGCTGAATCATGAAAAA 1647
RESULT 4
AAE21858
ID AAE21858 standard; DNA; 1197 BP.
XX
AC AAE21858;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 245.
XX
KW Human; breast cancer; cytosolic; immunosuppressive;
KW neutrophic; neurproliferative; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; antiviral; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN W020005173-1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-611515/58.
XX
DR P-PSDB: AAB58955.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
PS Claim 1; Page 669; 1299pp; English.
XX
CC Sequences AAE21614 - AAE22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAE22032 - AAE22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytotoxic; immunosuppressive;
CC neutrophic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antitumor; antiviral; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiac activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and agonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.
XX
SO Sequence 1197 BP; 230 A; 396 C; 350 G; 216 T; 5 other;

Query Match 63.8%; Score 1158.6; DB 21; Length 1197;
Best Local Similarity 99.3%; Pred. No. 2.4e-247;

Matches 1180: Conservative 3; Mismatches 3; Indels 2; Gaps 2;														
QY	624	CGGCTGCTTTACTGGCTGAGATCAACGCTGGCCCTGGGCCATCTCCACTCCAGGGCA	683	1703	GGGCGAGCTGTGCCCCGTGATATGAGCAGAGGCGCCGCCACACCCCGCTCAA	1762								
DB	11	CGGCTGCTTTACTGGCTGAGATCAACGCTGGCCCTGGGCCATCTCCACTCCAGGGCA	70	DB	1091	GGGCGAGCTGTGCCCCGTGATATGAGCAGAGGCGCCGCCACACCCCGCTCAA	1149							
QY	684	TCATCTACCGGAGCTTCAGCCCGAGACATCATGCTCAGACCGCAGGCCACATCAAC	743	QY	1763	CTGCTCCCGTGAAGATTAAAGGCTGATCATGAAAAA	1810							
DB	71	TCATCTACCGGAGCTTCAGCCCGAGACATCATGCTCAGACCGCAGGCCACATCAAC	130	DB	1150	CTGCTCCCGTGAAGATTAAAGGCTGATCATGAAAAA	1197							
QY	744	TGACGACTTTGACTCTGCAAGAGTCTATCCATGAGGCGCGCTCATCACACTTCT	803	RESULT 5										
DB	131	TGACGACTTTTGAAGCTGCAAGAGTCTATCCATGAGGCGCGCTCATCACACTTCT	190	ID	AAx61282	standard; cDNA: 1637 BP.								
QY	804	GGGCAACCATTTGAGTACATGGCCCCG-AGATTCTGTGTGGCAGTGGCCAAACCGGGCT	862	XX	AAx61282;									
DB	191	GGGCAACCATTTGAGTACATGGCCCCG-AGATTCTGTGTGGCAGTGGCCAAACCGGGCT	250	DT	29-JUL-1999	(first entry)								
QY	863	GTGGACTGTGGAGCTGGGGGCGCTGATATGACATGCTCACTGGATGCGCCCTT	922	XX	Human signal peptide-containing protein encoding cDNA SEQ ID NO:10.									
DB	251	GTGGACTGTGGAGCTGGGGGCGCTGATATGACATGCTCACTGGATGCGCCCTT	310	XX	Human; signal peptide-containing protein; SP; cell proliferation;									
QY	923	ACCGCAGAGAACCGGAAGAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCC	982	KW	cancer; neuronal disorder; immune response; detection; ss.									
DB	311	ACCGCAGAGAACCGGAAGAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCC	370	XX	Homo sapiens.									
QY	983	CCCTACCTACCCAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCAGC	1042	PN	WO924463-A2.									
DB	371	CCCTACCTACCCAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCAGC	430	XX	20-MAY-1999.									
QY	1043	CAGCGATTGGGGGTGGCCAGGGGATGCTGCTGATGTGTGAGAGACATCCCTTTCCGG	1102	PF	04-NOV-1998;	98WO-US23578.								
DB	431	CAGCGATTGGGGGTGGCCAGGGGATGCTGCTGATGTGTGAGAGACATCCCTTTCCGG	490	PR	07-NOV-1997;	97US-0966316.								
QY	1103	CACATGATTTGGGACGACCTTTCTGCGTGGCGATGAGACATCCCTTTCCGG	1162	PA	(INCY-) INCYTE PHARM INC.									
DB	491	CACATGATTTGGGACGACCTTTCTGCGTGGCGATGAGACATCCCTTTCCGG	550	PI	Au-Young J, Lal P, Mathur P, Murry LE, Reddy R:									
QY	1163	CAGTCAGAGAGAGACGTGAGCCAGTTTGAATACCGCTTTCACACGAGCAGCCGCTGGAC	1222	DR	WPI: 1999-337694/28.									
DB	551	CAGTCAGAGAGAGACGTGAGCCAGTTTGAATACCGCTTTCACACGAGCAGCCGCTGGAC	610	XX	cDNA clones encoding signal peptide-containing proteins									
QY	1223	AGTCGATGATCAACAGCCCTTCAGAGAGTCCCAACAGGCTTCTGGGCTTCACTAC	1282	PT	Claim 4; Page 75-76; 83pp; English.									
DB	611	AGTCGATGATCAACAGCCCTTCAGAGAGTCCCAACAGGCTTCTGGGCTTCACTAC	670	XX	The present sequence represents a human cDNA clone encoding a signal									
QY	1283	GTGGCGCGCTGCTCTCTGAGACATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGGCG	1342	CC	peptide-containing protein (SP). SP proteins can be used to stimulate									
DB	671	GTGGCGCGCTGCTCTCTGAGACATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGGCG	730	CC	cell proliferation or to treat or prevent cancer. SP antagonists are									
QY	1343	TCACCCAGGCGCTCAACAGTAGACCCCGGGTCCCGTCAAGCCCTCAAGTTCTCCCT	1402	CC	also used to treat or prevent cancer, and also for treating or									
DB	731	TCACCCAGGCGCTCAACAGTAGACCCCGGGTCCCGTCAAGCCCTCAAGTTCTCCCT	790	CC	preventing neuronal disorders or immune responses. Polynucleotide									
QY	1403	TTTGAAGGGTTTGGGCCAGCCCGACCTGCGGAGCCCAACGAGTACTCTACTCCCA	1462	CC	sequences complementary to the SP-encoding polynucleotides are useful									
DB	791	TTTGAAGGGTTTGGGCCAGCCCGACCTGCGGAGCCCAACGAGTACTCTACTCCCA	850	CC	for the detection of SP-encoding nucleic acid molecules in biological									
QY	1463	CTCTCTCAACCGCGCGCTCTGACACACGCGCTCTCCCTCAATCGTCCCGCTCAGGG	1522	XX	samples.									
DB	851	CTCTCTCAACCGCGCGCGCTCTGACACACGCGCTCTCCCTCAATCGTCCCGCTCAGGG	910	SO	Sequence 1637 BP; 342 A; 473 C; 463 G; 332 T; 27 other;									
QY	1523	ACCAAGAGTCTCAAGAGGGCGCTGGGCGTCAAGGGCGCTAGAGAACCGGGTGGGGTGA	1582	Query Match 60.8%; Score 1104.4; DB 20; Length 1637;										
DB	911	ACCAAGAGTCTCAAGAGGGCGCGTGGGCGTCAAGGGCGCTAGAGAACCGGGTGGGGTGA	970	Best Local Similarity 98.8%; Pred. No. 2.7e-235;										
QY	1583	GGGTACCTTTGAGCCTTCTCTGCGGCTGTAGAGACAGAGACCTTGAGCACTTCC	1642	Matches 1196; Conservative 0; Mismatches 7; Indels 8; Gaps 8;										
DB	971	GGGTACCTTTGAGCCTTCTCTGCGGCTGTAGAGACAGAGACCTTGAGCACTTCC	1030	QY	97	CGGGGGGGCGGGCGCGCCATGGCGCGCGTGTGATTGATTGGATTGAGACGAGGAGAG	156							
QY	1643	AGAGACCTGGGGGTGTGTGTGGGGGTGGGGGTGTGAGTGGTATGAAGGTGTGTGCT	1702	DB	176	CAGCGAGGCGGAGGCGGAGCAGAGCTCAGCCCGCGAGCAGATGCTCCCTTGGCGAGTT	216							
DB	1031	AGAGACCTGGGGGTGTGTGTGGGGGTGGGGGTGTGAGTGGTATGAAGGTGTGTGCT	1090	DB	236	CAGCGAGGCGGAGGCGGAGCAGAGCTCAGCCCGCGAGCAGATGCTCCCTTGGCGAGTT	295							

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OY 337 CAAGGGGGCTATGCGCAAGGTGTCAGGTGCGAAAGGTGCAAGGCACCAACTTGGGCA 396
    |||
DB 416 CAAGGGGGGCTATGCGCAAGGTGTCAGGTGCGAAAGGTGCAAGGCACCAACTTGGGCA 475
OY 397 AATATATGCCATGAAAGTCTTAAGAGAGGCCAAAATTTGCGCAATGCCAAGACAGC 456
    |||
DB 476 AATATATGCCATGAAAGTCTTAAGAGAGGCCAAAATTTGCGCAATGCCAAGACAGC 535
OY 457 ACACACAGGGGCTGAGCGGAGACATCTAGAGTCAGTGAAGCACCCTTTATGTGGAAGT 516
    |||
DB 536 ACACACAGGGGCTGAGCGGAGACATCTAGAGTCAGTGAAGCACCCTTTATGTGGAAGT 595
OY 517 GGGCTATGCTTTCAGACTGGTGGCAAACTTACTCACTTCTT-GAGTCCCTCAGTGGTG 575
    |||
DB 596 GGGCTATGCTTTCAGACTGGTGGCAAACTTACTCACTTCTTGGATTTGCTCCTCAGTGGTG 655
OY 576 GCGAGCTTTCACGCAATCTGAGAGCGAGAGGGGCAATCTTCTGGAAGATACGGCTCTCT 635
    |||
DB 656 GCGAGCTTTCACGCAATCTGAGAGCGAGAGGGGCAATCTTCTGGAAGATACGGCTCTCT 715
OY 636 ACCTGGCTGAGATCAAGCTGGGCTGGGCTGCTCCTCCTCCAGGGCATCTACCGGG 695
    |||
DB 716 ACCTGGCTGAGATCAAGCTGGGCTGGGCTGCTCCTCCTCCAGGGCATCTACCGGG 775
OY 696 ACCTCAAGCCCGAGAAATCATGCTCAGAGCGAGGGCCACATCAAACTGAGCCGACTTTG 755
    |||
DB 776 ACCTCAAGCCCGAGAAATCATGCTCAGAGCGAGGGCCACATCAAACTGAGCCGACTTTG 835
OY 756 GACTCTGCAAGAGATCTATCCATGAGGGGCGGCTACTCACAACCTTCTGCGGACCATTTG 815
    |||
DB 836 GACTCTGCAAGAGATCTATCCATGAGGGGCGGCTACTCACAACCTTCTGCGGACCATTTG 895
OY 816 AGTACATGGCCCTGAGATCTGAGTGGCGAGTGGCCACAACCGGGCTGTGAGCTGTGGA 875
    |||
DB 896 AGTACATGGCCCTGAGATCTGAGTGGCGAGTGGCCACAACCGGGCTGTGAGCTGTGGA 955
OY 876 GCGTGGGGCCCTGATGATACGATGCTCAGATGCGGCGGCTTTTACCGAGAGAAC 935
    |||
DB 956 GCGTGGGGCCCTGATGATACGATGCTCAGATGCGGCGGCTTTTACCGAGAGAAC 1015
OY 936 GGAAGAAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCCCTTACTCACCC 995
    |||
DB 1016 GGAAGAAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCCCTTACTCACCC 1075
OY 996 CAGATGCCCCGGGACCTTGTCAAAAAGTTCTTAAACGGAATCCAGCCAGCGGATTTGGGG 1055
    |||
DB 1076 CAGATGCCCCGGGACCTTGTCAAAAAGTTCTTAAACGGAATCCAGCCAGCGGATTTGGGG 1135
OY 1056 GTGGGCCAGGGGATGCTGCTGATGTGACAGAGATCCCTTTTTCGGGCAATGAATTTGGG 1115
    |||
DB 1136 GTGGGCCAGGGGATGCTGCTGATGTGACAGAGATCCCTTTTTCGGGCAATGAATTTGGG 1195
OY 1116 AGGACCTTCTGCGCTGGGCTGTGAGACCCCTTTTC-AGGCCCTGTCTGTGAGTCAGAGAG 1174
    |||
DB 1196 AGGACCTTCTGCGCTGGGCTGTGAGAGCCCTTTTCAGAGCCCTGTGTGAGTCAGAGAG 1253
OY 1175 GACGTGAGGCAATTTGATACCGGCTTTCACAGCGGAGAGCGCGGTGAGCATCTGATGAC 1234
    |||
DB 1234 GACGTGAGGCAATTTGATACCGGCTTTCACAGCGGAGAGCGCGGTGAGCATCTGATGAC 1312
OY 1235 ACAGCCCTCAGGAGAGTGGCCAAACAGGCGCTTCTGGGCTTCACTACCTGAGCGCGGT 1294
    |||
DB 1313 ACAG-CTCTCAGGAGAGTGGCCAAACAGGCGCTTCTGGGCTT-ACATTAAGTGGCGC-GTCT 1369
OY 1295 GTCTGTGAGAG 1305
    |||
DB 1370 GTCTGTGAGAG 1380

```

RESULT 6
AAZ87837
ID AAZ87837 standard; cDNA; 1607 BP.

```

XX AC AAZ87837;
XX XX
DT 19-JUN-2000 (first entry)
DE Human serine/threonine protein kinase (HSTK)-2 encoding cDNA.
KW Serine/threonine protein kinase; HSTK; cancer; leukemia; testicular;
KW melanoma; inflammatory disease; asthma; atherosclerosis; aniridia;
KW diabetes mellitus; growth disorder; anemia; achondroplastic dwarfism;
KW human; HSTK-3; HSTK-2; ss.
OS Homo sapiens.
XX XX
FH Key location/Qualifiers
FH CDS 101..1588
FT /tag=a
FT /transl_except=(pos:125..127, aa: Xaa)
FT /transl_except=(pos:140..142, aa: Xaa)
FT /transl_except=(pos:152..154, aa: Xaa)
FT /transl_except=(pos:200..202, aa: Xaa)
FT /transl_except=(pos:209..211, aa: Xaa)
FT /transl_except=(pos:221..223, aa: Xaa)
FT /transl_except=(pos:224..226, aa: Xaa)
FT /transl_except=(pos:290..292, aa: Xaa)
FT /transl_except=(pos:296..298, aa: Xaa)
FT /transl_except=(pos:305..307, aa: Xaa)
FT /transl_except=(pos:314..316, aa: Xaa)
FT /product="HSTK-2"
FT /note="Xaa = unknown"

W0200015770-A2.
PD 23-MAR-2000.
XX XX
PF 16-SEP-1999; 99WO-US21595.
XX XX
PR 16-SEP-1998; 98US-0153939.
XX XX
PA (INCY-) INCYTE PHARM INC.
XX XX
PI Bandman O, Tang YT, Goli SK, Corley NC, Guegler KJ, Gorgone GA;
PI Hillman JL;
XX XX
DR WPI: 2000-271413/23.
DR P-PSDB: AAY77844.
XX XX
PT Human serine/threonine protein kinases useful in the prevention,
PT diagnosis and treatment of cancers, inflammatory diseases and disorders
PT that affect growth and development -
XX XX
PS Disclosure: Fig 1A-E; 73pp; English.
XX XX
CC The invention relates to human serine/threonine protein kinase (HSTK)
CC polypeptides and the nucleic acids that encode them. The HSTK-3 protein
CC can be expressed by standard recombinant methodology. The HSTK-3
CC polypeptides may be used as antigens in the production of antibodies
CC against HSTK-3 and in assays to identify modulators (agonists and
CC antagonists) of HSTK-3 expression and activity. The HSTK-3 specific
CC antibodies and modulators can be used to treat disorders such as cancers
CC (e.g. leukemia, testicular cancer and melanoma), inflammatory diseases
CC (e.g. asthma, atherosclerosis and diabetes mellitus) and disorders that
CC affect growth and development (e.g. anemia, achondroplastic dwarfism and
CC aniridia). The anti-HSTK-3 antibodies may also be used as diagnostic
CC agents for detecting the presence of HSTK-3 polypeptides in samples (e.g.
CC by enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents a cDNA encoding a HSTK-2 polypeptide.
XX XX
SQ Sequence 1607 BP; 312 A; 519 C; 472 G; 283 T; 21 other;

```

Query Match 39.6%; Score 720; DB 21; Length 1607;
Best Local Similarity 99.1%; Pred. No. 4.7e-150;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Db 584 GAGAGGGAATATTTATGGAAGACATGCTGCTTTACTTTGGCAGAAATCTCCATGCTT 643
QY 660 TGGGCACTCCATCCCGGGGATCATACCGGGACCCGAGCAATCATATG 719
Db 644 TGGGGCTTTACTTCAAAAGGGATCTTACAGAGCTGGAAGCCGGAAATATCTG 703
QY 720 TCAGCAGCCAGGGCCATCAACTGACGACTTTGGACTCTGCAAGAGACTATCAG 779
Db 704 TTAATCAACCAAGTCAATGTGAATCAACAGACTTTGGACTATGCAAAAGATATCATG 763
QY 780 AGGCGCCGCTCACTCACTCTTGGGGACCAATTGATACATGCGCCCTGAGATTCTG 839
Db 764 ATGGAACAGACACACACATTTTGTGGAACAATAGAAATGAGCCCTGGAATCTTGA 823
QY 840 TGGCAGTGGCCACACCGGGCTGTGGACTGTGGAGCCCTGGGGCCCTGATGACACA 899
Db 824 TGAGAAATGGCCCAATCTGCTGTGTGATTTGTGGAGTTTGGAGCAATTAATGATGACA 883
QY 900 TGGTCACTGGATGCGCGCCCTTTACCGCAGAGAACCGGAAGAAACCATGATAGATCA 959
Db 884 TGGTGAATGGAGACCCCATTCATGCGGAGAGAAATAGAAAGAAACAATGACAAATCC 943
QY 960 TCAGGGGCAAGCTGGCAGCTGCCCCCTACTCAACCCAGATGCCCGGAGCTTGTCAAA 1019
Db 944 TCAAAATGTAACTCAATTTGCTCCCTCACTCAACAAAGAACGAGATCTGTTAAA 1003
QY 1020 AGTTTCTGAACGGAATCCACAGCAGCAGATTTGGGGGTGGCCAGGGGATGCTGTGATG 1079
Db 1004 AGCTGCTGAAGAAAGAAATGCTGCTTCTGCTGGAGCTGCTCGGGAGCTGGAGAAAG 1063
QY 1080 TGCAGAGACATCCCTTTTCCGGACATGAAATTTGGAGCACTTCTGGCCCTGGCGTGG 1139
Db 1064 TTCAAGCTCATCATCTTTAGACACATTAACGTGGAAAGAACTTGTGCGAAAGGTGG 1123
QY 1140 ACCGCCCTTACAGCCCTGCTGTGACATGACAGAGAGAGAGCTGAGCCAGTGTGATACC 1199
Db 1124 AGGCCCCCTTTAAACCTGTGTGCAATCTGAAGAGATGAACTGTTGATTTCCAAAT 1183
QY 1200 TCACAGGAGAGAGCGGCTGGAGAGTCTGTATGACACAGCCCTCAGGAGAGAGCCAAAC 1259
Db 1184 TTACAGCTGAGACACCTGTGACAGCCCAATGATCACTCAAGTGAAGAGTCCCAATC 1243
QY 1260 AGGCTTCTCTGGCTTCACTACATGCTGGCGGCTGTCTGTGACAGAGCATCAAGAGGCT 1319
Db 1244 AGGTCTTCTGGCTTTTACATATGTGGCTCATCTGTGAAGTGAAGAAAGT 1303
QY 1320 TCCCTTCCAGCCCAAGCTGCGCTCAACCCAGGGGCTCAACAGATAGCCCGGCTCCCG 1379
Db 1304 TTTCTTTGAAACCAAAATCCGATCACTCGAAGATTATTTGGCAAGCCCAACACCTG 1363
QY 1380 TCAGCCCTCTCAAGTCTCCCTTTTGA 1407
Db 1364 TCAGCCAGTCAAAATTTCTCTCGGGGA 1391

RESULT 9
ABLI1561
ID ABL1561 standard; DNA; 1898 BP.
XX
AC ABL1561:
XX
XX 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1156.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.

PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 1156; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABLI1840-ABLI3011), expressed DNA
CC sequences (ABLI737-ABLI2072).
CC (ABSI737-ABSI2072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1898 BP; 520 A; 496 C; 496 G; 386 T; 0 other;
Query Match 28.3%; Score 514; DB 23; Length 1898;
Best Local Similarity 67.9%; Pred. No. 2, 3e-104;
Matches 718; Conservative 0; Mismatches 340; Indels 0; Gaps 0;
QY 261 AGCTGACTGAGACACAGCTGAGACGTTGGCCAGAGGCGATGGGCCCTGTTGAGC 320
Db 176 AGCTTGGCAGAGAAATGTTAATCCAGTAAATCAAGCTGGAGCCAAAGACTTTGAGC 235
QY 321 TGTGCGTGTGCTGGGCAAGGGGCTATGCGAAGTGTTCAGTGGCAAGGTGCAAG 380
Db 236 TCAAGAAAGCTCTTGGCAAGGTGTATGCGAAATATTTTCAGGTGCGCAAGCCGTG 295
QY 381 GCACCAACTGGGCAAAATATATGTCATGAAGTCTTAAGGAAGGCCAAATTTGCGCA 440
Db 296 GAGCAGATGCTAACAAATATTTTGCATGAAGTGTCTCAAAAAGCATCATGTGTACCA 355
QY 441 ATGCCAAGGACACAGACACAGCGGCTGAGCGGAACATTTAGATCAAGTGAACACC 500
Db 356 ATCAAAAGGACACAGGACACACCGCGGAGCGCAATATACGAGGACATCAACATC 415
QY 501 CCTTATTTGGAACATGCGCTATGCTTCCAGACTGTGGCAAACTCACTCACTCTG 560
Db 416 CTTTCATATGAGGAGTATGCTTCCAGCAACAGGAAATATACCTTATATCTTG 475
QY 561 AGTGCCTAGTGTGAGCGAGCTCTTCAAGCATGTGAGGAGGAGCATCTTCTGGAAG 620
Db 476 AATATCTCAGCGGTGGAGAGCTGTTCATGATTTTGAAGCGTGAGGAGCATCTTCTGAGG 535
QY 621 ATAGGCTGCTTCTAATGCTGTGAGATCAAGCTGGCCCTGGGCAATCTCCACTCCAG 680
Db 536 ATACCAATGCTCTTATTTAAAGGAATCATTTTGGCCTTGGGCAATCAACAACTGG 595
QY 681 GCATCATCTACGGGAGCTCAACCCGGAAGACATCATGCTCAAGACAGGAGGCAATCA 740
Db 596 GCATCATCTACCGGAGCTGAAGCCCGAAGAACTACTGCTGATGACAGAGGAGCATGA 655
QY 741 AACTGACCGAATTTGGACTGTCAAGAGAGTCTATCCATGAGGAGGCGGCTCACTCACT 800
Db 656 AGCTCAGGACTTCCGAGCTGTCAAGAGGACACATCAAGAGGATATTTGACCCACACCT 715

QY 801 TCTGGGACCATTTAGTACATGCCCCCTGAGATTCTGGTCCGACGACCAACCGGG 860
D 716 TCTGGGACCATTTAGTACATGCCCCCTGAGATTCTGGTCCGACGACCAACCGGG 775
QY 861 CTGGAGCTGGTGGAGCCTGGGGCCCTGATGTACAGCATCTCACTGATGCGCCCT 920
D 776 CAGTCGCTGGTGGTCACTGGGCGCTGATGTGATGATCTCAAGAGTCCCACT 835
QY 921 TTACCGAGAGAACCGGAAACCATGATGATCATGAGGCGCAAGCTGGCATGC 980
D 836 TCACCGCGAGAAATCGCAAGAAAGCATGAGACCATCTGAAGCCAGCTCAATCTGC 895
QY 981 CCCCCCTCCTACCCAGATGCCCCGAGCTGTCTCAAAAAGTTCTGAACGGAATCCA 1040
D 896 CAGCTACCTCACAACCGGAGCCAGGATCTGTGCTGCGCTGATGAAGCGGAGAAC 955
QY 1041 GCCAGCGATTTGGGGGTCGGCCAGGGATGCTGATGTGACAGAGATCCCTTTTCC 1100
D 956 CTCAGCGCTTGGAGCGGACCGGAGATGCGGGGCTTCAATACACCCATTCTTCA 1015
QY 1101 GGCACATGATTTGGGACGACCTTCTGGCTGGCTGGACCCCTTTCAGGCGCTGC 1160
D 1016 AACACGTCACTGGGAGCATGTGCTCGCCAGACGCTGAGCCGCTTAAACCGCTCT 1075
QY 1161 TGCAGTCAGAGAGAGAGCTGAGCAATTGATACCCGCTTACACGAGACGCGGTGG 1220
D 1076 TGAGAGCGAGAGATGATGTCTACAGATTGATACAGATTCACAAGCAAAATTCAGTGG 1135
QY 1221 ACAGTCTGATGACACACGCCCTCAGCCAGATGCTCCACACGAGCCCTTCTGGCTTCAAT 1280
D 1136 ATTACCTGATGATGATCAACGCTTAAGCGAAAGTCAATTTAATTTTCCAAAGGTTTCACT 1195
QY 1281 ACGTGGCGCTGTCTGTGAGACAGCATCAAGAGGCG 1318
D 1196 ACCTTGGACCTCGATACCTGAGAGGATGATCGGGCC 1233

RESULT 10
AAV19873
ID AAV19873 standard; DNA; 2556 BP.
XX AAV19873;
XX 23-JUN-1998 (first entry)
XX Drosophila p70S6k gene.
DE Drosophila p70S6k gene.
XX p70S6k; p70 S6 kinase; enzyme; kinase signalling pathway; ss.
XX Drosophila melanogaster.
FH Key Location/Qualifiers
FT CDS 474..2387
FT /*tag= a
PN WO9803662-A2.
PD 29-JAN-1998.
PE 11-JUL-1997; 97WO-EP03680.
PR 24-JUL-1996; 96GB-0015498.
XX (NOVS) NOVARTIS AG.
PI Kozma S, Stewart M, Thomas G;
XX WPI: 1998-120783/11.
DR P-PSDB; AAM52294.
XX New isolated Drosophila p70 S6 kinase - is used to develop products
PT for studying the kinase signalling pathway and for modulating the
PT kinase activity

XX Claim 3; Page 38-42; 47pp; English.
PS This sequence encodes the Drosophila p70 S6 kinase (p70S6) of the
XX invention. The products are used in the study of the p70 S6 kinase
CC enzyme. They can be used for defining the p70 S6 kinase signalling
CC pathway and to develop agents for modulating the kinase activity. The
CC products can also be used for the production of antibodies and for
CC detection.
XX
SQ Sequence 2556 BP; 717 A; 663 C; 643 G; 533 T; 0 other:
Query Match 28.3%; Score 514; DB 19; Length 2556;
Best local similarity 67.9%; Pred. No. 2.5e-104;
Matches 718; Conservative 0; Mismatches 340; Indels 0; Gaps 0;
QY 261 AGCTGACTGAGACCGCTGACGTTGGCCCAAGCCGATGGGCCCCACTGCTTGAAC 320
D 649 AGCTGCGAGAGAGATTTAATCCAGGTAAATCAAGCTGGAGCCCAAGGACTTTGAGC 708
QY 321 TGCTGCTGTGGGCAAGGGGGCTATGGCAAGGTGTTCCAGTGCGAAAGTGCAAG 380
D 709 TCAGAAAGTCTTGGCAAGGCGGTATGCGAAAGTATTTAGTGGCGCAAGACCGTG 768
QY 381 GCACCACTTGGGCAAAATATATGCGATGAAAGTCTTAAGAAAGCCAAATTTGCGCA 440
D 769 GACGAGATGCTAACAAATATTTTGCATGAAGGTGCTCAAAAAGCATTCATGTGACCA 828
QY 441 ATGCCAAGACACACACACACAGCGGCTGAGCGGAACATTTTAAGTCAAGTGAAGCAC 500
D 829 ATCAAAAGAGACACACGACGACCCGCGGAGCGGCAAAATCTCAGGACGACGACATC 888
QY 501 CTTTATTTGGAACTGGCCTATGCTTCCAGACTGGTGGGCAAACTTACCTCATCTTG 560
D 889 CTTTATGTTGAGGCTAGTTTATGCTTCCAGACGACGAGAAATATATCTTATCTTG 948
QY 561 AGTGCCTAGTGTGGCGAGCTCTTACAGCATCTGAGACGAGAGGCAATCTTCTGGAAG 620
D 949 AATATCTCAGCGGTGAGAGCGTTCATGTCATTTGAGACGTGAGGCAATCTTCTGAAG 1008
QY 621 ATACGGCTGCTTCTACCTGGCTGAGATCAGCTGGCCCTGGCCATCTCCACTCCAGG 680
D 1009 ATACCATGCTTCTATCTAAGCGAAATCATTTTGGCCCTGAGCATACCAAACTGG 1068
QY 681 GCATCATCTACCGGAGCTCAAGCCGAGAAATCATGCTCAAGCCGAGGGCCACACA 740
D 1069 GCATCATCTACCGGAGCTCAAGCCGAGAAATCATGCTCAAGCCGAGGGCCACACA 1128
QY 741 AACTGACCGACTTTGACTCTGCAAGAGTCAATCATGAGGCGCCCTCACTCACTCACCT 800
D 1129 AGCTCAGGACTTTGACTCTGCAAGAGACATCAAGAGGCTTGTCTACCCACACT 1188
QY 801 TCTGGGCAACATTTGATGATGCGCCCTGAGATTTCTGTGCGGACGAGCCAAACCGGG 860
D 1189 TCTGGGCAACATTTGATGATGCGCCCTGAGATTTTTCACGAGAGTGGCCATGGCAAG 1248
QY 861 CTGTGAGCTGTGAGCCTGGGGCCCTGATGTACAGATGCTCACTGATGCGCCCT 920
D 1249 CAGTCGCTGGTGGTCACTGGGCGCTCTCATGTGTGATGATGCTCAAGAGTCCACCT 1308
QY 921 TTACCGAGAGAACCGGAAACCATGATGATCATGAGGCGCAAGCTGGCATGC 980
D 1309 TCACCGCGAGAAATCGCAAGAAAGCATGAGACCATCTGAAGCCAGCTCAATCTGC 1368
QY 981 CCCCCCTCCTACCCAGATGCCCCGAGCTGTCTCAAAAAGTTCTGAACGGAATCCA 1040
D 1369 CAGCTACCTCACAACCGGAGCCAGGATCTGTGCTGCTGCTGAAGCGGAGAAC 1428
QY 1041 GCCAGCGATTTGGGGTGGCCAGGGATGCTGCTGATGTGAGAGATCCCTTTTCC 1100
D 1429 CTCAGCGCTTGGAGCGGACCGGAGATGCGGGGCTTCAATTAACCATCTTCTCA 1488
QY 1101 GGCACATGAAATTTGGAGACCTTCTGGCCTGGCTGTGAGACCCCTTTTCAGGCGCTGTC 1160

DB 1489 AACACGTCAGACGGAGCGATGTGCTCGCCAGACGCCCTCCAGCCGCTATTAACCCCTCTC 1548
OY 1161 TGCAGTCAGAGGAGGAGCGAGCAGTTTGATACCCGCTTCACAGCGAGCGCGGTG 1220
DB 1549 TCGAAGACGAGGATGTGCTCTCACAGTTCGATACAAAGATTCCAAATTCAGGTG 1608
OY 1221 ACAGTCTGATGACACAGCCCTCAGCGAGAGTCCCAACCAAGCCCTTCGCGCTTCACAT 1280
DB 1609 ATTCCCTGATGATACAAAGCGTAAAGGAAATTTAATTTTCCAAAGGTTTACCT 1668
OY 1281 ACGTGCGCCGCTCTCTCTGCGACAGCATCAAGAGGCG 1318
DB 1669 ACGTTGCACTCTGATACGAGAGATATGCATCGGCGC 1706

RESULT 11
AAH77989
ID AAH77989 standard; DNA; 843 BP.
XX
AC AAH77989;
XX
DT 13-NOV-2001 (first entry)
DE Partial nucleotide sequence of human protein kinase SGK216.
XX
KW Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW brain disease; neuronal disease; Alzheimer's disease; chromosome 17;
KW Parkinson's disease; multiple sclerosis; metabolic disorder;
KW peripheral nervous system disease; amyotrophic lateral sclerosis;
KW infection; ocular disease; migraine; pain; sexual dysfunction;
KW mood disorder; attention disorder; cognition disorder; hypotension;
KW hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO20016594-A2.
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US06838.
XX
PR 06-MAR-2000; 2000US-0187150.
PR 29-MAR-2000; 2000US-0193404.
PR 13-NOV-2000; 2000US-0247013.
XX
PA (SUGEN) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
DR WPI; 2001-536777/59.
DR P-PSDB; AAG67390.
XX
PT Nucleic acids capable of encoding human polypeptides having a kinase or
PT kinase-like activity, useful for diagnosing a disease selected from
PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT Alzheimer's disease) -
XX
PS Example 1; Fig 1A; 201pp; English.

The present sequence encodes a partial human protein kinase. The
gene is located at chromosomal position 17q21.2-q22. The kinase
polypeptides are useful for diagnosing a disease or disorder
selected from cancers (e.g. cancers of tissues and cancers of
hematopoietic origin), immune-related diseases and disorders,
cardiovascular disease, brain or neuronal-associated diseases (e.g.
Alzheimer's disease, Parkinson's disease, multiple sclerosis),
metabolic disorders, peripheral nervous system diseases, amyotrophic
lateral sclerosis, viral infections, infections caused by prions,
infections caused by bacteria, infections caused by fungi, ocular
diseases, migraines, pain, sexual dysfunction, mood disorders,
attention disorders, cognition disorders, hypotension, hypertension,
psychotic disorders, dyskinesias, and organ transplant rejection.

CC Kinase inhibitors are useful for treating diseases and disorders
CC described above.
XX
SQ Sequence 843 BP; 268 A; 173 C; 187 G; 215 T; 0 other;
Query Match 25.1%; Score 455.6; DB 22; Length 843;
Best Local Similarity 72.0%; Pred. No. 1.7e-91;
Matches 609; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

OY 425 GCCAAATTTGTGGCAATGCAAGGACAGACACAGCGGGCTGAGGCAATCTTA 484
DB 1 GCATATATGTAAGAAATCTTAAGATACAGCTCATACAAAAGCAGAAATATTCTG 60
OY 485 GAGTCAGAGACCCCTTTATTTGGAAGTGGCCCTTCCAGTCCAGTGTGCAAA 544
DB 61 GAGGAAGTAAGGATCCCTTCATTTGGAATTAAGCTTAATGCTTCCAGCTGTGAAA 120
OY 545 CTCTACCTATCTTGAAGTGCCTCAGTGTGGGAGCTTTCACGATCTGGAGGAG 604
DB 121 CTCTACCTATCTTGAAGTGCCTCAGTGTGGGAGGAACTATTATGAGTTAGAAAGAG 180
OY 605 GGCATCTTCGGAAGATACGGGCTGCTTACCTGCGAGATACGCTGGCGCTGGCG 664
DB 181 GGAATATTTATGGAAGACAGCTGCTGCTTTTACTTGGCAAGAAATCTCATGGCTTTGGA 240
OY 665 CATCTCAGTCCAGGGGCAATCTACCGGAGCTTCAGCCGAGAAATCATGCTCAGC 724
DB 241 CATTTACATCAAAAGGGATATCATATACAGACCTGAAACCGGAGAAATCTTAAAT 300
OY 725 AGCGAGGCGACATCAACTGACCGCACTTTGAGCTGTGCAAGAGTCTATCCATGAGGC 784
DB 301 CACCAAGGTCATATGAAATACAGACTTTGGACTTGGCAAGAAATCTTTCATGATGA 360
OY 785 GCGGCTACTACACCTTCTGCGGACCATTTGAGTACATGAGCCCTGAGATTCGAGGCC 844
DB 361 ACAGTACACACACATTTTGTGAGACAAATAGATATGAGCCCTGAAATCTTGAATGA 420
OY 845 AGTGCCACAAACCGGCTGTGAGTGTGAGAGCTGGGGCCCTGATGACGATGCTC 904
DB 421 AGTGCCACAAATGCTGCTGTGAGTGTGAGAGTGTGAGAGTATTAATGATGACATGCTG 480
OY 905 ACTGAGTCCGCCCTTTACCGCAGAGAAACCGAAGAAACCATGATTAAGATCATCAG 964
DB 481 ACTGAGACACCCCATTTACTGGGAGAAATGAAAGAAACCAATGACAAATCTCTCA 540
OY 965 GGCAGCTGAGACTGCCCCCTACTCACCCGAGATGCCCGGAGCTTGTCAAAAAGTTT 1024
DB 541 TGTAACTCAATTTGCTCTCTACCTACACAAAGAACGAGATGCTGTTAAAGAGCTG 600
OY 1025 CTGAAACGGAATCCAGCCAGCGGATTTGGGGTGGCCAGAGGATGCTGATGTGAG 1084
DB 601 CTGAAAGAAATCTGCTCTCTC---TGGAAGCTGGTCTGGGAGCCTGAGAAAGTTCAA 657
OY 1085 AAGCATCCCTTTTCCGAGCATGAATTTGGAGAGCACTTCTGGCCCTGGAGTGGACCC 1144
DB 658 GCTCATCAATTTCTTGAACATAATTAAGGAGAACTTCTGGCTCAAAAGGTGGAGCC 717
OY 1145 CCTTCAGGCCCTGTCTGAGTACAGAGAGAGAGTACGACATTTGATACCCGCTTCACA 1204
DB 718 CCTTTAAACCTCTGTGCAATCTGAAGAGATGATGAATGATTTATTTCAAGTTTACA 777
OY 1205 CGGACAGCGCCGCTGAGACGCTGATGACACAGCCCTCAGCGAGAGTCCAAACGAGCC 1264
DB 778 CGTCAACAGCTGTGACAGGCCAGATGACGAAATCTCAGTAAACTGCATTCAGATCAGT 837
OY 1265 TTCCTG 1270
DB 838 TTCCTG 843

RESULT 12
AAK86891
ID AAK86891 standard; DNA; 4357 BP.

XX AAK86891;
AC
XX 07-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41703.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
XX MO200157182-A2.
PD
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 14-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 03-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

QY 1646 GACCTGGGGGTGTCTGTGGGGGTGGGTGTGAGTCCGTAAAGAAAGTGTGTCTGTCTGGG 1705
|||||
DB 6766 GACCTGGGGGTGTCTGTGGGGGTGGGTGTGAGTCCGTAAAGAAAGTGTGTCTGTCTGGG 6825
QY 1706 GCAGCTGTGCCCTGAAATCATGGGACAGGAGGGGCGCCGACACCCCGCGCTCACTG 1765
|||||
DB 6826 GCAGCTGTGCCCTGAAATCATGGGACAGGAGGGGCGCCGACACCCCGCGCTCACTG 6885
QY 1766 CTCCTCGTGAAGATTTAAAGGGCTGAATCATG 1796
|||||
DB 6886 CTCCTCGTGAAGATTTAAAGGGCTGAATCATG 6916

RESULT 14
ABK64273
ID ABK64273 standard; DNA: 445 BP.
XX
AC ABK64273;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #168.
XX
KW Human: benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN MO200212440-A2.
XX
PD 14-FEB-2002.
XX
PE 07-AUG-2001; 2001MO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX
PI Mungier WE, Kulikarni P, Getzenberg RH, Waga I, Yamamoto J;
PI
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure: Page 131; 444pp; English.
XX
XX The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX

SO Sequence 445 BP; 72 A; 163 C; 125 G; 85 T; 0 other;
Query Match 23.1%; Score 418.8; DB 24; Length 445;
Best Local Similarity 99.1%; Pred. No. 2e-83;
Matches 442; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1043 CAGCGGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGAGAGACATCCCTTTTCCGG 1102
|||||
DB 2 CAGCGGATTTGGGGGTGG-CCAGGGGATGCTGCTGATGTGAGAGACATCCCTTTTCCGG 60
QY 1103 CACATGAATTTGGGACGACCTTCTGGCCCTGGGTGGAGACCCCTTTCAGGCCCTGTCTG 1162
|||||
DB 61 CACATGAATTTGGGACGACCTTCTGGCCCTGGGTGGAG-CCCTTTCAGGCCCTGTCTG 119
QY 1163 CAGTCAGAGGAGGACGTCGACCCAGTTTGAATCCCGCTTCACAGGACGAGCCGGTGGAC 1222
|||||
DB 120 CAGTCGAGGAGGACGTCGACCCAGTTTGAATCCCGCTTCACAGGAGGAGCCGGTGGAC 179
QY 1223 AGTCCTGATGACACAGCCCTCAGCGAGAGTGCACACAGGCGCTTCTGGGCTTCACATAC 1282
|||||
DB 180 AGTCCTGATGACACAGCCCTCAGCGAGAGTGCACACAGGCGCTTCTGGGCTTCACATAC 239
QY 1283 GTGGCGCCGTCGTGCTGCGAGACATCAAGAGGGGCTTCCTTCAGGCCCAAGCTGGCG 1342
|||||
DB 240 GTGGCGCCGTCGTGCTGCGAGACATCAAGAGGGGCTTCCTTCAGGCCCAAGCTGGCG 239
QY 1343 TCACCCAGGCGCCTCAACAGTAGCCGCCGGTCCGCTCAGCCGCCCTCAAGTTCTCCCT 1402
|||||
DB 300 TCACCCAGGCGCCTCAACAGTAGCCGCCGGTCCGCTCAGCCGCCCTCAAGTTCTCCCT 359
QY 1403 TTTGAGGGGTTTGGGCCACCCAGCCTCGCGAGGCCACGAGACTACTTACTCCCA 1462
|||||
DB 360 TTTGAGGGGTTTGGGCCACCCAGCCTCGCGAGGCCACGAGACTACTTACTCCCA 419
QY 1463 CTCCTGCCACGGCGCGCCCTCGAC 1488
|||||
DB 420 CTCCTGCCACGGCGCGCCCTCGAC 445

RESULT 15
AAFI5983
ID AAFI5983 standard; cDNA: 673 BP.
XX
AC AAFI5983;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SRO ID NO:418.
XX
KW Human: prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
XX Homo sapiens.
OS
PN MO200055174-A1.
XX
PD 21-SEP-2000.
XX
PE 08-MAR-2000; 2000MO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56780.

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 20:57:05 ; Search time 2070 Seconds

(without alignments)
3872.834 Million cell updates/sec

Title: US-09-762-258-2

Perfect score: 2614

Sequence: 1 MARGRRARGAAMAAPVFL.....PIRPPSTKSKRGGRGR 495

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human4.0.cdi -LIST=45
-OCALIGN=200 -THR.SCORE=DCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-XGAPOP=10 -YGAPEXT=0.5 -Delop=6 -Delext=7

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Database :

EST:*

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2:	em_estchum:*
3:	em_estlin:*
4:	em_estlmu:*
5:	em_estcov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hlc:*
9:	gb_estl:*
10:	gb_estl2:*
11:	gb_hlc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2391.5	91.5	1834	11	AK014412	AK014412 Mus muscu
2	1648.5	63.1	992	9	AL529444	AL529444 AL529444
3	1574	60.2	1076	14	BM923000	BM923000 AGENCOURT
4	1569.5	60.0	1037	14	BM059474	BM059474 AGENCOURT
5	1543.5	59.0	1014	14	BM052654	BM052654 AGENCOURT
6	1541.5	59.0	1005	14	BM423942	BM423942 AGENCOURT
7	1511.5	57.8	943	14	BM643418	BM643418 AGENCOURT
8	1493.5	57.1	1075	14	BM062171	BM062171 AGENCOURT
9	1481	56.7	952	14	BM918927	BM918927 AGENCOURT
10	1477	56.5	1049	14	BM642404	BM642404 AGENCOURT
11	1477	56.5	1048	14	BM052262	BM052262 AGENCOURT
12	1454	55.6	849	9	AL527983	AL527983 AL527983
13	1448.5	55.4	923	14	BM890823	BM890823 AGENCOURT
14	1426	54.6	1176	14	BM061526	BM061526 AGENCOURT
15	1422.5	54.4	1049	14	BM054269	BM054269 AGENCOURT
16	1421.5	54.4	1018	14	BM057747	BM057747 AGENCOURT
17	1408.5	53.9	1080	14	BM062488	BM062488 AGENCOURT
18	1387	53.1	834	12	BM792760	BM792760 AGENCOURT
19	1387	53.1	895	9	AL521570	AL521570 AL521570
20	1376.5	52.7	1044	14	BM072582	BM072582 AGENCOURT
21	1353.5	51.8	883	14	BM877063	BM877063 AGENCOURT
22	1351.5	51.7	997	14	BM048653	BM048653 AGENCOURT
23	1333	51.0	854	14	BM0431606	BM0431606 AGENCOURT
24	1331	50.9	891	12	BM829030	BM829030 AGENCOURT
25	1328	50.8	850	9	AL560524	AL560524 AL560524
26	1325	50.7	793	13	BM907389	BM907389 AGENCOURT
27	1324.5	50.7	789	9	AL525066	AL525066 AL525066
28	1323.5	50.6	867	13	BM1821158	BM1821158 AGENCOURT
29	1318.5	50.4	865	12	BM792968	BM792968 AGENCOURT
30	1318	50.4	764	12	BM673589	BM673589 AGENCOURT
31	1312	50.2	1109	14	BM058742	BM058742 AGENCOURT
32	1306	50.0	1082	13	BM561338	BM561338 AGENCOURT
33	1301	49.8	757	13	BM1084346	BM1084346 AGENCOURT
34	1288	49.7	767	9	AL519476	AL519476 AL519476
35	1288	49.3	858	14	BM0961675	BM0961675 AGENCOURT
36	1287	49.2	899	14	BM0942698	BM0942698 AGENCOURT
37	1285	49.2	783	13	BM1825778	BM1825778 AGENCOURT
38	1281	49.0	814	12	BM488888	BM488888 AGENCOURT
39	1265.5	48.4	2957	11	AK012045	AK012045 Mus muscu
40	1264.5	48.4	1057	14	BM915476	BM915476 AGENCOURT
41	1254	48.0	757	13	BM020218	BM020218 AGENCOURT
42	1251.5	47.9	842	12	BM797272	BM797272 AGENCOURT
43	1230	47.1	780	13	BM224008	BM224008 AGENCOURT
44	1226	46.9	896	12	BM799643	BM799643 AGENCOURT
45	1226	46.9	1152	14	BM052906	BM052906 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS AK014412
DEFINITION Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830402N06;protein tyrosine phosphatase, receptor type, C
ACCESSION AK014412
VERSION AK014412.1
KEYWORDS GI:12852247
SOURCE HTC: CAP trapper.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS		Carninci, P. and Hayashizaki, Y.
TITLE		High efficiency full-length cDNA cloning
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)
MEDLINE		99279253
PUBMED		10349636
REFERENCE	2	
AUTHORS		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL		Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE		prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED		Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	3	
AUTHORS		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
TITLE		Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
JOURNAL		Sun, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A.,
MEDLINE		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, T.,
PUBMED		Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K.,
REFERENCE	4	
AUTHORS		Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J.,
TITLE		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL		RIKEN integrated sequence analysis (RISA) system--384-format
MEDLINE		sequencing pipeline with 384 multiplexed sequencer
PUBMED		Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	5	
AUTHORS		Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
TITLE		Arkawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
JOURNAL		Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
MEDLINE		Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,
PUBMED		Kadota, K., Matsuda, H., Asbunuer, M., Batalov, S., Casavant, T.,
REFERENCE	6	
AUTHORS		Fleischmann, N., Gaasterland, T., Gissi, C., King, B., Kochwa, H.,
TITLE		Kuehl, P., Lewis, S., Matsuno, Y., Nikaido, I., Pesole, G.,
JOURNAL		Quackenbush, J., Schriml, L. M., Stebbins, F., Suzuki, R., Tomita, M.,
MEDLINE		Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
PUBMED		Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, A.,
REFERENCE	7	
AUTHORS		Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
TITLE		Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
JOURNAL		Hotmann, M., Hume, D. A., Kamlay, M., Lee, N. H., Lyons, P.,
MEDLINE		McDonnell, L., Mashima, J., Mazzarelli, J., Momberts, P., Nordone, P.,
PUBMED		Ringo, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
REFERENCE	8	
AUTHORS		Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H.,
TITLE		Toyo-Oka, K., Wang, K. H., Wetz, C., Whiteker, C., Wilming, L.,
JOURNAL		Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.
MEDLINE		and Hayashizaki, Y.
PUBMED		Functional annotation of a full-length mouse cDNA collection
REFERENCE	9	
AUTHORS		Nature 409 (6821), 685-690 (2001)
TITLE		21085660
JOURNAL		11217851
MEDLINE		5 (bases 1 to 1834)
PUBMED		Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
REFERENCE	10	
AUTHORS		Arkawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
TITLE		Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T.,
JOURNAL		Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
MEDLINE		Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
PUBMED		Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,
REFERENCE	11	
AUTHORS		Kubhara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
TITLE		Nunakata, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
JOURNAL		Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D.,
MEDLINE		Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
PUBMED		Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
REFERENCE	12	
AUTHORS		Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yamanaka, I.,
TITLE		Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
JOURNAL		Hayashizaki, Y.
MEDLINE		Direct Submission
PUBMED		Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
REFERENCE	13	
AUTHORS		Physical and Chemical Research (RIKEN), Laboratory for Genome
TITLE		Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
JOURNAL		RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
MEDLINE		Kanagawa 230-0045, Japan (E-mail: genome-res@gc.riken.go.jp).
PUBMED		

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAAATCTCGAGTTAATTAAATATCCCCCCCCC 3']. cDNA was prepared by using Trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAAATCTCGAGTTAATTAAATATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from lambda FLIC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

Location/Qualifiers

1. 1834

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/strain="C57BL/6J"

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/db_xref="MGD:MGI:1903117"

/db_xref="taxon:10090"

/clone="3830402N06"

/sex="female"

/tissue_type="placenta and extra embryonic tissue"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="18 days pregnant adult"

1. 1834

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80. 1537

/note="Ptpcrap"

/note="data source:MGD, source key:MGI:97811, evidence:ISS protein tyrosine phosphatase, receptor type, C polypeptide-associated protein putative"

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BASE COUNT 432 a 527 c 512 g 363 t

ORIGIN

Alignment Scores:

Pred. No.: 1,24e-186 Length: 1834

Score: 2391.50 Matches: 454

Percent Similarity: 94.55% Conservative: 14

Best local Similarity: 91.72% Mismatches: 24

Query Match: 91.49% Indels: 3

DB: 11 Gaps: 1

US-09-762-258-2 (1-495) x AK014412 (1-1834)

0Y 4 GYARGATGALAAAGGLYALAGLYALALAAETHALAAVALAHPHEASPLEUASPLEUGLU 23

DB 50 GGCCAAAGGCTCCCGGAGACCGGGGGCCCATGCGCGCCGATTTGATTAGACTTGAG 109

0Y 24 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 43

DB 110 ACCGAGGAAGGAGACGAGGCGGAGGCGGACACCGAGTTTCAACCCCTTCGCGAGCTGTGTC 169

QY 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeu 63
 DB 170 CTGGCGCAATTAAAGGCGCTGCTGCGGAGACAGTGGGACATATGACAGAAAGTAGAGCTG 229
 QY 64 ThrGluThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeu 83
 DB 230 ACAGAGACAGCGGTGACCTGGCTGAGCGCATCGGGCCACCTGCTTGAGGCTACTG 289
 QY 84 ArgValLeuGlyGlyGlyGlyTyrGlyValPheGluValArgGlyValGlyGlyThr 103
 DB 290 AGCTGACGGGAGAGGGGCTATGGCAGGTGTTCCAGGTGAGAAAGTGAAGGACAC 349
 QY 104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
 DB 350 AACTGGGAAAAATATATGCTTGAAGGTCTTAAGGAGGCCAGATTATGACAGTGC 409
 QY 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
 DB 410 AAGGACACAGCCCATACCGGGCTGAGAGAACATTCTGAAATCTGTGAAGCATCCCTTC 469
 QY 144 IleValGluLeuAlaTyrAlaPheGluThrGlyLysLeuTyrIleLeuGluCys 163
 DB 470 ATTGTAGAACTGGCTATGCTTCCAGACAGGTGGCAAACTGCTCATCTCGAGTGC 529
 QY 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThr 183
 DB 530 CTCATGCTGGGTGAGCTCTTCACACATCTTGAGCGAGAAAGCATCTCTCGAGACACA 589
 QY 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
 DB 590 GGCTGCTCTACCTGGCAGAGATCAACACTAGCCCTGGCCATCTCCATCCACGGCATT 649
 QY 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
 DB 650 ACTCTACCGGACCTCAAGGCTGAGAACATCATGCTCAGCAGCGGCCACATCAAACTG 709
 QY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGlyAlaValHisThrPheCys 243
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 QY 244 GlyThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
 DB 770 GGCACCATGAGTACATGCGCCAGAGATTAGTCCGACATGTCACAACCGGGCAGTG 829
 QY 264 AspTyrPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePheThr 283
 DB 830 GACTGTGAGGCTGGAGACCTGATGTACGACATGCTCAGTGGATCGCCCTTCACT 889
 QY 284 AlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysAlaLeuProPhe 303
 DB 890 GGAGGAAACCGGAGAAACCTATGGATTAATTAAGGAAAGCTGTGCTGCCCCC 949
 QY 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGln 323
 DB 950 TACCTCACCCCGGATGCCGGGACCTTGCCAAAAGTTCTGAAGCGGAACCCCACTAG 1009
 QY 324 ArgIleGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHis 343
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QY 404 AlaProSerValLeuAspSerIleLeuGlyGluPheSerPheGluProLysLeuArgSer 423
 DB 1250 GCACCTTGTCTCTGGACAGCATCAAGAGGGCTTCTCTTCCAGCCCAAGCTGGCTTCT 1309
 QY 424 ProArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPhe 443
 DB 1310 CCCAGACGCGCTTAACAGCAGTCCCGCCACCCCATCAGCCCTCAAGTTCTTCCCTTT 1369
 QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuLeuProProLeu 463
 DB 1370 GAGGGGTTCGGCCCAAGTCCCGCCACCAAGAGCCCATGAGCCATCTTACCTCCACTC 1429
 QY 464 Leu-----ProProProProProSerThrThAlaProLeuProIleArgProPro 480
 DB 1430 CTACCATCAACACCATCACACACACACACACACACACACACACACACACACACAC 1489
 QY 481 SerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
 DB 1490 TCAGGAACCAAGAACGTCAGAAAGGAGCGGCGCTCAGGCGGT 1534
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 LOCUS AL529444 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD006YE23 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL529444
 VERSION AL529444.1 GI:12792937
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 992)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
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 /sex="male"
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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library of the pCMVSPORT 6 by life technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liliang@life.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 220 a 278 c 306 g 184 t 4 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.75e-126 Length: 992
 Score: 1648.50 Matches: 320
 Percent Similarity: 97.87% Conservative: 2
 Best Local Similarity: 97.26% Mismatches: 6
 Query Match: 63.06% Indels: 1
 DB: 9 Gaps: 1
 US-09-762-258-2 (1-495) x AL529444 (1-992)
 QY 8 ArgGlyAlaGlyAlaAlaMetAlaAlaValAlaPheAspLeuAspLeuGluThrGluGluGly 27

Db	5	CGGGG --- GGGGCGCCCATGGCGGGCCGGTGTGATTGGATTGGAGACGAGGAAGC	61
Qy	28	SerGIuGIyGluGIyLupProGIuLeuSerProAlaAspAlaCysProLeuAlaGIuLeu	47
Db	62	ACCGAGGGCGAGGGGAGGACGACAGCTCAAGCCCGCGAGCAGCTGTCCCTTCCAGATTG	121
Qy	48	ArgAlaAlaGIyLeuGIuLupProValGIyHisTyrGIuGIuValGIuLeuThrSer	67
Db	122	AGGGAGCTGGGCTTGAAGCTGTGGGACACTATGTAAGAAGTGGAGCTACATGAACACAGC	181
Qy	68	ValAsnValAlGIyProGIuArgTLeGIyProHisCysPheGIuLeuLeuArgValLeuGIy	87
Db	182	GTGAACGTTGGGCCAGAGCGCATCGGGGCCACTGTGGAGCTTGAAGCTCTGCGTGGGC	241
Qy	88	LysGIyGIyTyrGIyLysValPheGIuValArgLysValGIuGIyThrAsnLeuGIyLys	107
Db	242	AAGGGGGGCTATGGCAAGGTGTTCAGAGTGCAAGAGGTGCAAGGACACCACTGGGGCAA	301
Qy	108	IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla	127
Db	302	ATATATGCTATGAAGTCTTAAGAGGACCAAAATTTGGCGGMAATGCCAAGGACACACA	361
Qy	128	HisTyrArgAlaGIyArgAsnIleLeuGIuSerValLysHisProPheIleValGIuLeu	147
Db	362	CACACACGGGCTGACGCGGACATTTAGAGTCAGTTAAAGCACCCCTTATATGTGGAGCTG	421
Qy	148	AlaTyrAlaPheGIuThrGIyLysLeuTyrLeuIleLeuGIuLysLeuSerGIyLys	167
Db	422	GGCTATGGCTTCAGACATGTGTGGCAAACTCATCTCATCTTGAATCTCTCATGTGTGGC	481
Qy	168	GIuLeuPheThrHisLeuGIuArgLysLysIlePheLeuGIuAspThrAlaCysPheTyr	187
Db	482	GAGCATCTTCACCACTGTGGAGGACGAAGGCAATCTTCCTGGAAATACGGCCGTCTTAC	541
Qy	188	LeuAlaGIuIleThrLeuAlaLeuGIyHisLeuHisSerGIuGIyIleIleTyrArgAsp	207
Db	542	CTGGCTGAGATACGCTGGCCCTGGGCCCATCTCCACTCCAGGGCATCATCTTACCGGAGC	601
Qy	208	LeuLysProGIuAsnIleMetLeuSerSerGIuGIyHisIleLysLeuThrAspPheGIy	227
Db	602	CTCAAGCCCGAACAATCATGTCTGACAGACGCAAGGCGCAATCAATGACGACATTGGA	661
Qy	228	LeuCysLysGIuSerIleHisGIuGIyAlaValThrHisThrPheCysGIyThrIleGIu	247
Db	662	CTCTCAAGGAGTCTATCCATGAGGGCGCGCTCACTCAACCTTCTGGGGCACATTGAG	721
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Qy	268	LeuGIyAlaLeuMetTyrAspMetLeuThrGIySerProProPheThrAlaGIuAsnArg	287
Db	782	CTGGGGGGCCCTGATGTAGACATGCTCACTGATGTGGCCCTTTACCGCAGAGAACGG	841
Qy	288	LysLysThrMetAspLysIleIleArgGIyLysLeuAlaLeuProTyrLeuThrPro	307
Db	842	AAGAAACCATGATGAATCATCAAGGGGCAAGCTGGCACTGCCCTTACTTACCTCACCCA	901
Qy	308	AspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGIuArgIleGIyLys	327
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Db 344 AACTGGGCAAAATATATGCCATGAAAAGTCTTAAGGAAGGCCAAATTTGGCCCAATGCC 403
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Db 404 AAGGACACACACACACACGCGGCTGAGCGGAATCTTAAGTACAGTGAAGACCCCTTT 463
QY 144 ILevalGluLeuAlaTyrAlaPheGlnThrGlyGlyLysLeuTyrIleuIleGluCys 163
Db 464 ATGTGGAACTGGCCTATGCTTCACAGACTGGTGGCAAACTACCTACCTCATCTTGAAGTGC 523
QY 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThr 183
Db 524 CTCAGTGGTGGCAGCTCTTACAGCATCTGGAGCGAGAGGGCATCTTCCGGAAGATACG 583
QY 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
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Db 644 ATCTACGGGAGCTCAAGCCCGGAACATCATCTCAGACGAGGCCACATCAAACTG 703
QY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCys 243
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QY 244 GlyThrIleGlyIleThrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
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RESULT 4
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VERSION BQ059474.1 GI:19818814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1037)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LICM2070 row: 0 column: 22
High quality sequence stop: 611.
Location/Qualifiers
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/note="Organ: lymph. Vector: pORF7, site 1: XhoI, site 2:
EcoRI. cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 206 a 356 c 282 g 191 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2, 92e-119 Length: 1037
Score: 1569.50 Matches: 307
Percent Similarity: 96.86% Conservative: 1
Best Local Similarity: 96.54% Mismatches: 8
Query Match: 60, 04% Indels: 4
DB: 14 Gaps: 0

US-09-762-258-2 (1-495) x BQ059474 (1-1037)

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QY 200 SerGlnGlyIleIleTyrAlaAspLeuLysProGluAsnIleMetLeuSerSerGlnGly 219
Db 63 TCCAGGGGCAATCATCAACCGGACCTCAACCGGAAACATCATGCTCACACACCGGCGC 122
QY 220 HisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThr 239
Db 123 CACATCAAACTGACCCGACTTGGACCTGCAAGAGCTTTCATGAGGCGCCGCTACT 182
QY 240 HisThrPheCysGlyThrIleGlyIleTyrMetAlaProGluIleLeuValArgSerGlyHis 259
Db 183 CACACCTTGGCGGACACATTTGATGATGCGCCCTGAGATCTGGTGGCGCAGTGGCCAC 242
QY 260 AsnArgAlaValAspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
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QY 280 ProPhePheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeu 299
Db 303 CCGCCCTTCAACCCGACAGAACCCGGAACAAACATGATGATCATCAGGCGCAAGCTG 362
QY 300 AlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArg 319
Db 363 GCACCTGCCCCCTACCTCACCCCAAGATGCGCGGACCTTGTCAAAAAGTTTGTGAACGG 422
QY 320 AsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGlnArgHisPro 339
Db 423 AATCCAGCCAGCGAGTGGGTGGCCAGGGGATGCTCTGATGTGACAGACATCC 482
QY 340 PhePheArgHisMetAsnTrpAspAspLeuAlaIleTyrArgValAspProphePheArg 359
Db 483 TTTTTCGGGACATGAAATTTGGAGCAGACTTCTGGCTGGGTGGACCCCTTTCAGG 542
QY 360 ProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThr 379
Db 543 CCTGTCTGACAGTACAGAGGAGGAGTGTGAGCTTGTGATGATCCGCTTCACACGCGAGACG 602

QY	380	ProValaapSerProAspaSPthAlaLeuSerGIuSerAlaasngAlaAlaPheLeuGIy	399
Db	603	CCGGGGAGACAGCCCGATGACACACCCCTCAGCGAGATGGCCACACAGCCCTTCGGGC	662
QY	400	PheHrrYrValaAlaProSerValaLeuAspSerIleYsgIuGIyPheSerPheGIuPro	419
Db	663	TTCACTATACGTGGCGCCGCTGTCTCTGGACACATCAAGAGAGGCGTTCTCTTCAGGCC	722
QY	420	LysLeuArgSerProArGArGIuAsnSerSerProArGAlProValaSerProLeuLys	439
Db	723	AAGCGCCCTCACCCAGCGCCCTCAACAGTAGACCCCCCGCGGCCCGCTCAGCCCTCAAG	782
QY	440	PheSerProPheGIuGIyPheArGIuProSerSerProSerLeuProGIuProthGIuLeuPro	459
Db	783	TTCTCCCTTTTGAAGGGGTTTGGCCGACCCCAACCTGCGGACCCACGAGACTACT	842
QY	460	LeuProProLeuLeuProProProProSerThrrThrrAlaProLeuProIleArGIyPro	479
Db	843	CTACCTCA-CTCCTTCACAG- GCGGCGTCCTTGACACAGGCCCCCTCTCCATCGCTGCC	900
QY	480	ProSer-GlyThrIyLysLysSerLysArg-GlyArgGIyArGIyProGIyArg	495
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DEFINITION	AGNCOURT_6871884 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5934028		
ACCESSION	B0052654		
VERSION	B0052654.1	GI:19811994	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	EnkairYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 1014)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: rcgapsb@emall.nih.gov		
	Tissue Procurement: Dr. Daniel McVicar, DBS/NCI		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ILNL at:		
	http://lmgc.nih.gov		
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	/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:		
	EcoRI; CDNA made by oligo-dT priming. Directionally cloned		
	into EcoRI/XhoI sites using the following 5' adaptor:		
	GGCCAGAC(G). Library constructed by Ling Hong in the		
	Laboratory of Gerald M. Rubin (University of California,		
	Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and		
	Superscript II RT (Life Technologies). Note: this is a		
	NIH_MGC Library."		
BASE COUNT	225 a	312 c	278 g
ORIGIN			197 t
			2 others
Alignment Scores:	3.92e-117	length:	1014
Prod. No.:			

Score:	1543.50	Matches:	312
Percent Similarity:	86.03%	Conservative:	2
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Query Match:	59.05%	Indels:	33
DB:	14	Gaps:	2
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DB	1 GGTTCAGAGTGGCAAAAGGTGCAGAGGACACCACTTNGGCAAAATATATGCATGAAGT	60	
QY	113 LLEUARGYLSALALYSILEVALARGASNALALASPETHALAHSTRARGALAGUAT	133	
DB	61 CCTAAGGAAGGCCAAAATTGGCCCAATGCCCAAGACACAGACACAGGGGTGAGCG	120	
QY	133 GASNLLEUGLUSERVALYSHISPROPHILEVALGULEUVALATYRALAPHEGINTH	153	
DB	121 GACACTTTAGAGTCAGTGAAGACACCCCTTATTTGTGGAACTGGCCTATGCTTCCGAC	160	
QY	153 IGLYGLYLSLEUTRYLEUULEUGLUCYLSLEUSERGLYGLYGLULEUPHERTHRISE	173	
DB	181 TGGTGCAAAACHTACCTCATCTTTGAGTGCCCTCAGTGGTGCGAGCTCTTACGCACTCT	240	
QY	173 UGLUARGLUGLYILEPHELEUGLUASPTHALACYPHERTRYLEUALAGULIETHRLE	193	
DB	241 GGAGCGAAGAGGCACTCTTCCTGGAAGATACGGCTGCTTACTGCTGCTAGATCAGCT	300	
QY	193 UALALEUGLYHSLEUHSISERGLYILEICTYARGASPREUYSPROGUASNIL	213	
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QY	213 EWELEUSERSERGLINGLYHSILEYLSLEUTHRASPHEGLYLEUCYSLYSGUSERIL	233	
DB	361 CATGCTCAGACAGCCAGGCGCCACATCAACATGACCCAGCTTTGACTGCAAGGAGCTCAT	420	
QY	233 EHISGLUGLYALAVALTHRHISTRHPHECYGLYTHRIIEGLUTYRTHETALAPROGUUL	253	
DB	421 CCATGAGGGCGCGCGCATCACACTTCTGGGGACCATTAGTACATGGCCCTTGAGAT	480	
QY	253 ELEUVALARGSERGLYHSISANARGALAVALASPTRTPTSERLEUALLYALAEUWECTY	273	
DB	481 TCTGGTGGCGAGTGCCCAACCGGGCTGTGACTGGTGAGCCTGGGGGCCCTGATGTA	540	
QY	273 IASPELEUTHRGLYSERPROPROPHETHALAGUASNARGYLSYSTHRMETASPLY	293	
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QY	293 SILELLEARGLYLSLEUALALEUPROPTOTRYLEUTHRPROASPALARGASPLEUVA	313	
DB	601 GATCATCTACAGGGCAAGCTGGACACTGCCCTTACTCCTACCCCAATGATCCGGGACCTTGT	660	
QY	313 LLYSYSHETHEUYSARGASNPROSERGINARGILEGLYGLYLPROGLYASPALAAL	333	
DB	661 CAAAAAGTTTCTGAAAACGAATCCACGACACGGATGGGGGTGGCCAGGGGATGCTGC	720	
QY	333 AASPYALGINARGHISPROPHETHEARGHISMETASNTTPASPALEUUALATPAR	353	
DB	721 TGATGTGCAGAGACATCCCTTTTCCGGCACATGATATTTGGACACACTTGTGGCTGTGGC	780	
QY	353 GVALASPROPHETARGPROCYLSLEUGINSERGLUGLUASPYALSERGINPHEASPTH	373	
DB	781 TGTGAGACCCCTTTACAGGCCCTGTCTCAGTGCAGAGAGAGACGTGAGCCAGTTTGATAC	840	
QY	373 IARGPHERTHARGINTHRPROVAL-ASPSEPRIOASPASTHHALA-LEUSERGLUSER	392	
DB	841 CCGCTTTCACAGGCGAGAACCGGTGGGACACTCTGTATGACAGCCCTTCACAGAGAGT	900	
QY	393 ALA-ASNGLINAPHELEUGLYPHEHTHYVALALAPROSERVALLEUASPSERILELY	412	
DB	901 GCCCAACCAAGCGCCTT-----	916	
QY	412 SGLUUYLPHESERPHGINPROVYLSLEUARGSERPROARGTRGLUASNSERSEPROR	432	

Db	61	ACGGAGGAAGGACGAGGAGGCGAGGCGACGACAGCTCACGCCCGCGAGCATGTGCC	120
Oy	44	LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeu	63
Db	121	CTTGGCGAGTTGAGGGGAGCTGGCCCTTAAGGCTGTGGGACACTATGAAGAGGTGAGCTG	180
Oy	64	ThrGluThrSerValAsnValGlyProGluArgGlyLeuGlyProHisCysPheGluLeu	83
Db	181	ACTGAGACCAGCGTAACTGTGGCCCCAAGCGCATCGGGCCCCCACTGCTTTGAGCTGCTG	240
Oy	84	ArgValLeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGlnGlyThr	103
Db	241	CGTGCGTGGGCAAGGGGGGCGTATGGCAAGGTGTTCCAGGTGCGAAAGGTGCAGAGCAC	300
Oy	104	AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla	123
Db	301	AACCTGGGCAAAATATATAGCCATGAAAGTCCCTAAGGAAGAGGCCAAAATGTGGCGCAATCC	360
Oy	124	LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe	143
Db	361	AAGGACAGACGACACACACGGGCTGAGGGAACATTTGAGATCGTAGAAGCACCCCTTT	420
Oy	144	IleValIleLeuAlaTyrAlaPheGlnThrGlyGlyLysLeuTyrLeuIleLeuGluLys	163
Db	421	ATTGGGAACGTGGCTATGAGCCTTCACAGACTGGTGGCAAACTCTACCTCATCTTGAAGTC	480
Oy	164	LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThr	183
Db	481	CTCACTGGTGGGAGCTCTTCACGCATCTGGAGGAGGAGGATCTTCTCGAAGATACG	540
Oy	184	AlaCysPheTyrLeuAlaGluIlePheThrAlaLeuGlyHisLeuHisSerGlnGlyIle	203
Db	541	GCCTCCTTCTACCTGGCGAGATCACGCTGGCCCGGCGCCACATCTCCACGAGGCAATC	600
Oy	204	IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu	223
Db	601	ATCTACCGGAGACTAAGCCCGAGAACATCATGCTCAGACGACGAGGCCACATCAATG	660
Oy	224	ThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCys	243
Db	661	ACCGACTTTGGACGTGGCAAGGAGTCTATCCATGAGGGGCGCGTCACTCACACTTTCG	720
Oy	244	GlyThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal	263
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Oy	264	AspTrpTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThr	283
Db	781	GACTGTGTGAGGCTGGNGGGCCCTATGATGACACATGCTCACTGGATGGCGCCCTTCA	840
Oy	283	AlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeu--AlaLeuPr	302
Db	841	CGCAGAGAACCGGAAGAAACATGATGAAGTATCATCAGGGGGCAAGNCTGGGAGATGGCC	900
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DEFINITION AGNCNCOURT_8485261 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305404			
ACCESSION B0643418			
VERSION B0643418.1 GI:21767590			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

QY 5 ArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThr 24
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 Db 3 CGAGGGGCGCGCGGGCGCGCGCCATGCGCGCCCTGTTGATTGATTGGATTGGAGACG 62
 QY 25 GluGluGlySerGluGluGlyGluGluProGluLeuSerProAlaAspAlaGlyProLeu 44
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 QY 85 ValLeuGlyLysGlyGlyGlyGlyValPheGluValArgLysValGluGlyThrAsn 104
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 Db 243 GTGCTGGGCAAGGGGGCTATGGCGAGGTGTCCAGGTGGCAAGGTGCAAGGCACCAAC 302
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 Db 363 GACACAGCACACACACGCGCTGAGCGGAGACATTTCTAGAGTACAGTGAAGCACCCCTTATT 422
 QY 145 ValGluLeuValAlaThrAlaPheGlnThrGlyLysLeuThrLeuIleLeuGluCysLeu 164
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 Db 423 GTGGAACTGGCCTATGCTTCCAGACTGTGGCAAACTTCACTCATCTTGAAGTGCCTC 482
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 QY 185 CysPheThrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIle 204
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 Db 543 TGTCTTACCTGCTGAGTACGCTGCGCCCTGGCGCATCTCCATCCAGGGGCGATATC 602
 QY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThr 224
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 QY 225 AspPheGlyLeuGlyLysGluSerIleHisGluGlyAlaValAlaThrHisThrPheCysGly 244
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 DEFINITION 5', mRNA sequence.
 ACCESSION B0642404
 VERSION B0642404.1 GI:21766576
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 /note="Organ: lymph; Vector: pORF7; Site: 1: XhoI; Site: 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the Laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 BASE COUNT 203 a 276 c 300 g 169 t 1 others
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 Best Local Similarity: 95.18% Mismatches: 5
 Query Match: 56.50% Indels: 8
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 Db 28 GGGCGAGGGGCGCGCGGGCGCGCGCCATGCGCCCTGTTGATTGATTGGATTGGAG 87
 QY 24 ThrGluGluGlySerGluGluGlyGluProGluLeuSerProAlaAspAlaGlyPro 43
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 Db 88 ACGAGGAGAGCGAGCGGCGGAGGAGCCAGAGCTCAGCCCCGGGAGCGCATGTC 147
 QY 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisThrGluGluValGluLeu 63
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 Db 148 CTGGCGAGTTGAGGGGAGCTGAGCTAGAGCCCTGTGGACATATGAGAGGTGGAGCTG 207
 QY 64 ThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysPheGluLeu 83
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 Db 208 ACTGAGACCGCCTGGAACGTTGGCCAGAGCGCATGCGGCGCCACACTGCTTGGAGCTG 267
 QY 84 ArgValLeuGlyLysGlyGlyGlyGlyValPheGluValArgLysValGluGlyThr 103
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 Db 268 CGTGTGCTGGGCAAGGGGGCTATGGCGAGGTGTCCAGGTGGCAAGGTGCAAGGCACC 327
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 Db 328 AACTTGGGCAAAATATATGCGATGCAAGAAGTCTTAAGAGGCCAAANTGTGGCATGTC 387
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Db 388 AAGGACACAGCAGACACAGGGCTGAGCGAACAATCTAGATGACGTGAAGCACCCCTTT 447
OY 144 TLevalGluleuAlaTyraLapheGlnThrGlyGlyLeuTyrlleuLleuLucys 163
Db 448 ATTTGGAACTGGCCCTATCCCTTCCAGACTGGTGGCAAACTTACTCTCTTGATGTC 507
OY 164 LeuSerGlyGlyLeuLeuPheThrHisLeuGluArgGlyGlyLeuGluLeuGluLeu 183
Db 508 CTCATGGTGGGAGACTCTTACGACATCTGAGCGAGAGGAGCATCTCTCGAAGATACG 567
OY 184 AlaCysPheTyrlleuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyLe 203
Db 508 GCCTCTTCTACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627
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Db 628 ATCTACCGGGAGCTCAAGCCGAGAACATCATGCTCAGAGCCAGGCCAATCAAACTG 687
OY 224 ThrAspPheGlyLeuCysIleSerIleHisGluGlyAlaValThrHisThrPheCys 243
Db 688 ACCGACTTGGACTCTGCGAGAGTCTATCCATGAGGGGCGCTGCTGCTGCTGCTGCTG 747
OY 244 GlyThrIleGlyTyrcMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db 748 GGCACCATTTGAGTACATGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 807
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Db 808 GACTGTGGAGCTGGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 867
OY 283 rAlaGluAsnArg--LysIleThrMetAspLysIle-IleArgGly-----LysLe 299
Db 868 CGCAAGAAACCGGAAAGAAACCCCTGGGATGATGATGATGATGATGATGATGATGATGATG 927
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B0052262
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DEFINITION AGENCOURT_6868346 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933480
5', mRNA sequence.
ACCESSION B0052262
VERSION B0052262.1 GI:19811602
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1048)
NIH-MGC htcp://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LDCM2118 row: b column: 09
High quality sequence stop: 652.
Location/Qualifiers
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT 259 a 303 c 290 g 195 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1,21e+111 Length: 1048
Score: 1477.00 Matches: 299
Percent Similarity: 88.32% Conservative: 11
Best Local Similarity: 85.19% Mismatches: 27
Query Match: 56.50% Indels: 14
DB: 14 Gaps: 4
US-09-762-258-2 (1-495) x B0052262 (1-1048)
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Db 242 CGGAACATTTCTAGAGTCACTGAAGCACCCCTTATTTGTGAAGTGGCTTATGCTTCCAG 301
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OY 173 LeuGluArgGlyGlyIlePheLeuGluAspThrAlaCysPheTyrlleuAlaGluIleThr 192
Db 362 CTGGAGCGAGAGGGCATCTTCTGGAAGATACGGCTGTCTTACTGCTGATGATGATGATGATG 421
OY 193 LeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyraArgAspLeuTyrlleuGluAsn 212
Db 422 CTGGCCCTGGGCATCTCTCACTCCAGGCAATCATCTACCGGAGCTCAAGCCCGGAAC 481
OY 213 IleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLeuGlyCysIleSer 232
Db 482 ATCATGCTGACGACAGCGAGGCGCACATCAATCAATCAATCAATCAATCAATCAATCAATCA 541
OY 233 IleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGlyTyrcMetAlaProGlu 252
Db 542 ATTCATGAGGGGCGGCTGACTGACACCTTGTGGGCAACATGATGATGATGATGATGATGATG 601
OY 253 IleLeuValArgSerGlyHisAsnArgAlaValAspTrpTrpSerLeuGlyAlaLeuMet 272
Db 602 ATTTGTGTGCGCAGTGTGCACAAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 661
OY 273 TyrAspMetLeuThrGlySerProProPheThrAlaGluAsnArgLysTyrlleuMetAsp 292
Db 662 TACGACATCTCACTAGTATGATGCGCCCTTACCGGCAAGAACCGGCAAAACCATGATGAT 721
OY 293 LysIleIleArgGlyLysLeuAlaLeuProProTyrlleuThrProAspAlaArgAsp--- 311
Db 722 AAGATCATCAGGGGCAAACTGGCATGCGCCCTTACTCACCAGCAAAATGCGGGAACCT 781


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QY 312 LeuValLysLysPheLeuLysArgAsnProSerGlnArg-ILeGLyGLyProGlyAs 331
Db 782 TGTCAAAAAGTTTCTGTAAGAACGAAATCCACCAACGGAATGTGGGGTCCAGGGGA 841
QY 331 pAlaAlaAspVal-GlnArgHisProPhePheArgHisMet-AsnTPaPaAspLeuLeu 350
Db 842 AGCTGCTGGAAGTCCAAACATCCCTTTTCCGGCATGAATTTGGAAACAACCTTCTG 901
QY 351 -AlaTPaPArg---ValAspProPheArgProCysLeu-----GlnSerGlnGluAs 367
Db 902 GGCTGTGGGGGGGGGAGCCCTTTCAGGGCTTGTCTTCACCTCAAAAGGAAGAAC 961
QY 367 pValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThr 387
Db 962 TGGAAACCAATTGGA-----AACCCGCTTCCACCGGAAACAAAG 1003
QY 387 pAlaLeuSerGluSerAlaAsnGln 395
Db 1004 CCGGGGGGAACAGTCCCTGAATGAA 1028

RESULT 12
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LOCUS AL527983 LIT_NFL003_NBC3 Homo sapiens cDNA clone CS0DC027YH21 5
DEFINITION AL527983 Prime, mRNA sequence.
ACCESSION AL527983
VERSION AL527983.1 GI:12791476
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 849)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC027YH21"
/clone_1lb="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 178 a 242 c 268 g 159 t 2 others
ORIGIN

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QY 4 GlyArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGlu 23
Db 5 GGCCGACGGGGCCCGGGGGGGGGCCCATGGCCGCTGTGTTGATTTGGATTTGGAG 64
QY 24 ThrGlnGlnGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 43
Db 65 ACCGAGGAAGGACACCGAGGGCGAGGGCGAGCCAGAGCTCAGCCCGCGGACGATGTGCC 124
QY 44 LeuAlaGlnLeuArgAlaAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 63
Db 125 CTGGCCAGATTTGAGGGGAGCTGGGCTGAGAGCTGTGGGACATATGAAGAGGTGGAGCTG 184
QY 64 ThrGlnThrSerValAsnValGlyProGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGln 83
Db 185 ACTGAGACCAAGCGGGAAGCTGGGCGGAGAGCGGATCGGGCCCACTGCTTTGAGCTGCTG 244
QY 84 ArgValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 103
Db 245 CGTGTGCTGGGCGAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAGAGTCAAGGCAC 304
QY 104 AsnLeuGlnLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
Db 305 AACTGGGCAAAATATATGTCATGAAGAACTCTTAAGGAAGGCCAAATTTGGCCAATGCC 364
QY 124 LysAspThrAlaHisThrArgAlaGlnArgAsnIleLeuGlnSerValLysHisProPhe 143
Db 365 AAGGACACACACACACACGCGGTGAGCGGGAACATTTCTAAGTCAGTGAAGCACCCCTTT 424
QY 144 IleValGlnLeuAlaTyrAlaPheGlnThrGlnGlnLysLeuTyrLeuIleLeuGlnCys 163
Db 425 ATTGTGGAACTGGCTTATGCTTTCAGAGCTGTGGCAAACTCTTACCTCATTGAGTGC 484
QY 164 LeuSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 183
Db 485 CTCAGGTGTGGCGAGCTCTTCAGCAGCATGTGAGAGAGAGGAGGACTCTCGAAGATAG 544
QY 184 AlacysPheTyrLeuAlaGlnIleThrLeuAlaLeuGlnHisLeuHisSerGlnGlnIle 203
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QY 204 IleTyrArgAspLeuLysProGlnAsnIleMetLeuSerSerGlnGlnGlnGlnGlnGln 223
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QY 244 GlyThrIleGlnTyrMetAlaProGlnIleLeuValArgSerGlnHisAsnArgAlaVal 263
Db 725 GGCACTTGAATGATGATGAGCCCTGAGATTTCTGTGGCGCAGTGGCCAAACGGGGCTGTG 784
QY 264 AspTrpTrpSerLeuGlnGlnAlaLeuMetTyrAspMetLeuThrGlnSerProPheThr 283
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QY 284 Ala 284
Db 845 GCA 847

RESULT 13
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LOCUS B0890823
DEFINITION 5', mRNA sequence.
ACCESSION B0890823
VERSION B0890823.1 GI:22282837
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 923)

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US-09-762-258-2 (1-495) x AL527983 (1-849)


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      10 GGGCCAGCGGGCCGGGGGGCCGGCCGCGCATGGCGCGCGTGTGATTGGATTGGAG 69
OY      24 ThrGluGluGlySerGluGlyGluGluProGluLeuSerProAlaAspAlaCysPro 43
      70 ACGGAGGAAGGCGAGGCGGCGGCGGCGGAGCTCAGCCCGCGGAGCATGTCC 129
OY      44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisIstyrGluGluValGluLeu 63
      130 CTGGCGAGTTGAGGGCGAGCTGGCTAGAGCTGTGGGACACTATGAAGAGGTGAGCTG 189
OY      64 ThrGluThrSerValAsnValGlyProGluArgGlyIleGlyProHisCysPheGluLeuLeu 83
      190 ACTGAGACGACGAGTGAACGTTGGCCAGAGCCATCGGGCCCACTGCTTGAAGCTGCTG 249
OY      84 ArgValLeuGlyLysGlyGlyLysValPheGluValArgLysValGlnGlyThr 103
      250 CGTGTGTGGGCGAGGGGGCTATGGCAAGGTTCAGAGTGCAGAAAGGTGCAGAGCAC 309
OY      104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
      310 AACTGGGCAAAATATATGCCATGAAGTCTTAAGGAAGGCCAAATGTGCGCAATGCC 369
OY      124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
      370 AAGGACACAGCACACACACGCGCTAGCGGAACATTTAGACTCAGTGAAGCACCCCTTT 429
OY      144 IleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGluCys 163
      430 ATTGTGGAACGTGGCTATGCTTCCAGACTGGTGCAAACTTACCTCATCTTGAGTGC 489
OY      164 LeuSerGlyGlyGluLeuPheThrHisLeuGluValArgGluGlyIlePheLeuGluAspThr 183
      490 CTCAGTGTGGGAGCTCTTCACGATCTGAGCGAGGAGGCGATCTTCCTGGAAAGATAG 549
OY      184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
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OY      204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
      610 ATCTACCGGAGCTCAGCCGAGAACATCATGCTCAGACGCGGCGCACATCAACTG 669
OY      224 ThrAspPheGlyLeuGlySerIleHisGluGlyAlaValThrHisThrPheCys 243
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OY      244 GlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArg-AlaVal 263
      730 GGCACCATGTGAGTACATGCGCCCTAGATTCTGTGCGCAGTGGCACACCGGGGCTGT 789
OY      263 AspTrpTrp-SerLeuGlyAlaLeu-MetTyrAspMet-LeuThrGlySer--ProPr 281
      790 GGACTGAGTGAAGCTGGGGGCGCTGAGATGTACGACCTGGCTCAGTGGGAATCGCCGCC 849
OY      281 PheThrAlaGlu-AsnArgLysLysThr-MetAspLysIleIleArgGlyLysLeu--- 299
      850 TTTCCCGCGAGAAAACCGGAAAAAACCTTGATGATCTCAGGGGCAAACTGGGA 909
OY      300 AlaLeuProTyrLeuThrProAsp-AlaArg-AspLeuValLysLysPheLeuLys- 318
      910 ACTGCCCCCTTAACCTCAACCCCAATATGCCCCGGGACCTTGTCTCAAAAGTTTCCGANA 969
OY      319 --ArgAsnProSerGlnArg--IleGlyGlyGly--ProGlyAspAla 332
      970 ACCGATTCGCCACCCCGGAAATTGGGGGGGGGGCCCCCGGGAATGCC 1019
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 00:32:52 ; Search time 263 Seconds
(without alignments)
4238.552 Million cell updates/sec

Title: US-09-762-258-2
Perfect score: 2614
Sequence: 1 MARGRRAGCAAAVAEVDL.....PIRPPSGTKKSGRGRGRGR 495

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlh
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-DB=N.Geneseq_101002 -QFMT=fastlap -SUFPI=ring -MINMATCH=0.1 -LOOPL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09762258_ECGN_1.1_0.6runat_13112002_102444_4900 -KCPU=6 -ICPU=3
-NO_XLUPX -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONCLGO -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2614	100.0	1816	21	AAZ50703	p70(beta) S6 kinase
2	2594	99.2	1732	24	AAD37031	Human p54S6K DNA.
3	2371	90.7	1647	21	AAZ87838	Human serine/threo
4	1947.5	74.5	1637	20	AAK61282	Human signal pepti
5	1748	66.9	2346	24	ABL65827	Lung cancer relate
6	1646	63.0	1197	21	AAF21858	Human breast and o
7	1455	55.7	2556	19	AAH19873	Drosophila p70S6K
8	1447.5	55.4	1898	23	ABL16561	Drosophila melanog
9	1385.5	53.0	1607	21	AAZ87837	Human serine/threo
10	1385.5	53.0	1609	21	AAZ35657	Human serine/threo
11	1383	52.9	6923	22	AAK86892	Human immune/haema
12	1340	51.3	4357	22	AAK86891	Human immune/haema
13	1211.5	46.3	843	23	AAH77989	Partial nucleotide
14	1149	44.0	12396	23	ABL16560	Drosophila melanog
15	966	37.0	3061	24	ABK83808	Human cDNA differe
16	966	37.0	3061	24	ABN95648	Gene #2146 used to
17	961	36.8	2791	20	AAZ09173	Human rsk3 cDNA.
18	961	35.8	2791	20	AAK84493	p90 ribosomal S6 k
19	958	36.6	5673	24	AAK94865	Human DNA sequence
20	949.5	36.3	2260	17	AAT27730	Insulin-stimulated
21	949.5	36.3	2260	24	ABK84208	Human cDNA differe
22	948.5	36.3	2260	17	AAK27731	Human cDNA differe
23	937.5	35.9	2238	22	AAK44637	Mutant insulin-sti
24	934	35.7	3203	23	ABL25555	Novel protein kina
25	934	35.7	5656	23	ABL25554	Drosophila melanog
26	907.5	34.7	3120	21	AAK10529	Mitogen and stress
27	907.5	34.7	3225	21	AAZ46159	cDNA sequence enco
28	896.5	34.3	3400	22	AAK31952	Human polynucleoti
29	886.5	33.9	3131	21	AAK10533	Mitogen and stress
30	878.5	33.6	2134	21	AAK10543	Mitogen and stress
31	873.5	33.4	2116	21	AAK10542	Mitogen and stress
32	873.5	33.4	2117	21	AAK10531	Mitogen and stress
33	872.5	33.4	2134	21	AAK10530	Mitogen and stress
34	866.5	33.1	3132	22	AAK52936	Human polynucleoti
35	847	32.4	3165	23	AAK84870	DNA encoding novel
36	844	32.3	594	23	AAK19264	Human cDNA encodin
37	841.5	32.2	1230	23	AAK84869	DNA encoding novel
38	840	32.1	2222	21	AAK10532	Mitogen and stress
39	813.5	31.1	673	21	AAK15983	Human prostate can
40	810.5	31.0	1281	20	AAZ33647	Human breast tumou
41	806.5	30.9	1296	22	AAK4639	Novel protein kina
42	806.5	30.9	2346	20	AAV74190	Human sgk DNA. Ho
43	806.5	30.9	2370	19	AAV48311	Human cell-volume
44	806.5	30.9	2370	24	ABK84749	Human cDNA differe
45	806.5	30.9	2370	24	ABN97360	Gene #3858 used to

ALIGNMENTS

RESULT 1
AAZ50703
ID AAZ50703 standard: DNA; 1816 BP.

AAZ50703;
31-MAY-2000 (first entry)
p70(beta) S6 kinase gene.

p70 (beta) S6 kinase; p70betas6k; ribosomal protein kinase; S6 protein;
cellular signalling; probe; ribosomal activity; cellular proliferation;
cytostatic; ss.

OS Homo sapiens.
XX
XX Key
XX Location/Qualifiers
FT CDS 77..1564

|||||
Db 1397 TCCTCTTTGAGGGGTTTCGGCCAGCCAGCCGCGGAGCCACGAGGCTACTCTA 1456
OY 461 ProProLeuLeuProProProProSerThrThrAlaProLeuProLeuArgProPro 480
Db 1457 CCTCCACCTCCGCGCCCGCGCGCTCGACACCGCCCTCCATCCGTCGCCCC 1516
OY 481 SerGlyThrLysSerLysArgGlyArgGlyArgProGlyArg 495
Db 1517 TCAGGACCAAGAAAGTCCAAAGAGGGCCGTGGGCTCCAGGGCGC 1561
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ID AAD37031 standard; DNA; 1732 BP.
XX
AC AAD37031;
XX
XX 27-AUG-2002 (first entry)
XX
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XX
XX Human: mammalian kinase: p54S6K; p85S6K; antibody generation; cancer;
KM diagnosis; drug identification; cytosolic; enzyme; gene; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 36..1484
FT /*tag= a
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PN US6372467-B1.
XX
PD 16-APR-2002.
XX
PF 29-OCT-1999; 9905-0430564.
XX
PR 29-OCT-1998; 9805-106141P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Blenis J, Lee-fruman KK, Kuo CJ;
XX
XX WPI; 2002-424732/45.
DR P-PSDB; AAE23306.
XX
XX Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and
PT treating cancers -
PT
PS Example 1; Fig 1A; 30pp; English.
XX
XX The invention relates to mammalian kinases, p54S6K and p85S6K and
CC methods for identifying compounds that modulate, or which are modulated
CC by p54S6K and p85S6K. The p54S6K and p85S6K kinases may be used as
CC antigens to generate antibodies that may be used in immunoassays to
CC detect and quantitate the presence of p54S6K and p85S6K kinases in
CC samples and therefore be used to diagnose diseases, e.g. cancers. They
CC may also be used in assays as drug targets to identify potential drugs
CC for the treatment of diseases associated with p54S6K and p85S6K kinase
CC expression and activity. The present sequence is human p54S6K DNA.
XX
SQ Sequence 1732 BP; 355 A; 532 C; 532 G; 313 T; 0 other;
Alignment Scores:
Pred. No.: 9.86e-167 Length: 1732
Score: 2594.00 Matches: 491
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 24 Gaps: 0
US-09-762-258-2 (1-495) x AAD37031 (1-1732)

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Db 9 CGAGCGGCCCGCGGGGCGCGGCCCATGGCGGCGGTGGATTGGATTGGAGACG 68
OY 25 GluGluGlySerGluGlyGluGlyGluProGluLeuSerProAlaAspAlaCysProLeu 44
Db 69 GAGGAAGCAGCAGCAGCGGCGAGCGCAGCAGCTACGCCCGCGCAGCATGTCCTT 128
OY 45 AlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeuThr 64
Db 129 GCCAGTTGAGGGCAGCTGGCTAGAGCTGTGGAGACCTATGAAGAAGGTGAGCTGACT 188
OY 65 GluThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeuLeuArg 84
Db 189 GAGACACAGCTAAGCTTGTGGCCAGAGCGCATCGGCCCATGCTTTGAGCTGGCT 248
OY 85 ValLeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGluThrAsn 104
Db 249 GTGCTGGGCAAGGGGGGCTATGGCAAGGTGTCCAGTGTCCAAAGTGCMAAGGCACCAAC 308
OY 105 LeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
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OY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
Db 369 GACACAGCAGCAGACACAGCGGCTGAGCGGAACATTCTAGATGTCATAGACACCCCTTAT 428
OY 145 ValGluLeuAlaTyrAlaPheGluThrGlyLysLysLeuTyrLeuIleLeuGluCysLeu 164
Db 429 GTGGAACGTGGCTATGGCTTCCAGACTGGTGCMAAAGTCTATCCTGAGTGCCTC 488
OY 165 SerGlyLysGluLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThrAla 184
Db 489 AGTGTGGGAGCTGTCTTACGATCTGAGCGAGAGGAGCATCTTCTGGAAGATCGGCGC 548
OY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIle 204
Db 549 TGCTTCTACCTGCTGAGATCAAGCTGCGGCTGGGCGCATCTCCACGAGGATCAAC 608
OY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThr 224
Db 609 TACCGGAGCTTCAGACCCGAGAACATCATGCTCACACAGCCAGGCGCACATCAAACTGACC 668
OY 225 AspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheGly 244
Db 669 GACTTGGACTGTGCAAGAGTCTATCCATGAGGGCGCGCTGATCTACACCTTGTGGCGC 728
OY 245 ThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAsp 264
Db 729 ACCATTGAGTACATGGCCCTGAGATTCTGGTGGCGCAGTGGCCACACCGGGCTGTGAGC 788
OY 265 TyrTrpSerLeuGlyAlaLeuMetLysPheMetLeuThrGlySerProProPheThrAla 284
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OY 285 GluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProPhe 304
Db 849 GAAACCGGAAGAAAACCATGGATGAATCATCAGAGGGGCAACCTGGACATGCCCTTAC 908
OY 305 LeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGluArg 324
Db 909 CTCACCCCGAGATGCCCGGAGCTTGTCAAAAAGTTTCTGAACGGATGCCAGCCAGCGG 968
OY 325 IleGlyLysGlyProGlyAspAlaAlaAspValGluArgHisProPhePheArgHisMet 344
Db 969 ATTGGGGGGGCGCCAGAGGAGTCTGCTGATGTGSCAGACATACCTTTTTCGGGACATG 1028
OY 345 AsnTrpAspAspLeuLeuAlaThrParGlyLaaProProPheArgProCysLeuGlnSer 364
Db 1029 AATTGGAGCAGACTTGTGGCTGGCGTGGAGCCCGCTTATAGGCCCTGTGTGACATGA 1088
OY 365 GluGluAspValSerGluPheAspThrArgPheThrArgGluThrProValAspSerPro 384

```
|||||
DB 1089 GAGGAGGAGCTGAGCCAGTTGATACCCGCTTACACAGCGAGAGCCGGGAGAGTCTT
QY 385 AspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAla 404
DB 1149 GATGACACAGCCCTCAGCAGAGAGTGCACACAGAGCCCTTCTGGGCTTCACATACGTGGCG 1208
QY 405 ProSerValLeuAspSerTlelyGlyGlyPheSerPheGlnProLysLeuArgSerPro 424
DB 1209 CCGTCGTCTCTGAGACATCAAGGAGGCGCTTCTCCCTCCAGCCCAAGCTGCGCTCACCC 1268
QY 425 ArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu 444
DB 1269 AGCGCCCTCAGACATGAGCCCGCGGCTCCCGTACAGCCCTCAAGTCTCCCTTTTGAG 1328
QY 445 GlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeuLeu 464
DB 1329 GGGTTTCGGCCGACCCACACCTGCGGAGCCACGAGAGTACTCTACTCTCCACTCTCTG 1388
QY 465 ProProProProProSerThrThrAlaProLeuProLleArgProProSerGlyThrLys 484
DB 1389 CCACCGCGCGCGCTCGACACACCGCCCTCTCCCTCCGTCGCCCTCAGGGAGCCAG 1448
QY 485 LysSerLysArgGlyArgGlyArgProGlyArg 495
DB 1449 AAGTCCAGAGGGGCGGTGGGCGTCCAGGGGCG 1481
RESULT 3
AA287838
ID AA287838 standard; cDNA; 1647 BP.
AC AA287838;
XX
XX 19-JUN-2000 (first entry)
DE Human serine/threonine protein kinase (HSTK)-3 encoding cDNA.
XX
XX Serine/threonine protein kinase: HSTK; cancer; leukemia; testicular;
KW melanoma; inflammatory disease; asthma; atherosclerosis; aniridia;
KW diabetes mellitus; growth disorder; anemia; achondroplastic dwarfism;
KW human; HSTK-3; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 389..1405
FT /*tag= a
FT /*product= "HSTK-3"
XX
XX WO200015770-A2.
XX
XX 23-MAR-2000.
XX
XX 16-SEP-1999; 99WO-US21595.
XX
XX 16-SEP-1998; 98US-0153939.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Tang YT, Goli SK, Corley NC, Guegler KU, Gorgone GA;
PI Hillman JL;
XX
XX WPI; 2000-271413/23.
XX
XX P-PSDB; AAY77845.
XX
XX Human serine/threonine protein kinases useful in the prevention,
PT diagnosis and treatment of cancers, inflammatory diseases and disorders
PT that affect growth and development -
XX
XX Claim 9; Fig 2A-E; 73pp; English.
XX
XX The invention relates to human serine/threonine protein kinase (HSTK)-3
XX polypeptides and the nucleic acids that encode them. The HSTK-3 protein
```

```
CC can be expressed by standard recombinant methodology. The HSTK-3
CC polypeptides may be used as antigens in the production of antibodies
CC against hstK-3 and in assays to identify modulators (agonists and
CC antagonists) of hstK-3 expression and activity. The HSTK-3 specific
CC antibodies and modulators can be used to treat disorders such as cancers
CC (e.g. leukemia, testicular cancer and melanomas), inflammatory diseases
CC (e.g. asthma, atherosclerosis and diabetes mellitus) and disorders that
CC affect growth and development (e.g. anemia, achondroplastic dwarfism and
CC aniridia). The anti-hstK-3 antibodies may also be used as diagnostic
CC agents for detecting the presence of hstK-3 polypeptides in samples (e.g.
CC by enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents a cDNA encoding a HSTK-3 polypeptide.
XX
XX Sequence 1647 BP; 334 A; 507 C; 505 G; 299 T; 2 other;
```

Alignment Scores:

Pred. No.:	1,17e-151	Length:	1647
Score:	2371.00	Matches:	463
Percent Similarity:	94.128	Conservative:	1
Best Local Similarity:	93.918	Mismatches:	3
Query Match:	90.708	Indels:	27
DB:	21	Gaps:	3

US-09-762-258-2 (1-495) x AA287838 (1-1647)

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QY 5 ArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThr 24
DB 1 CGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 56
QY 25 GluGluGlySerGluGluGlyGluGluProGluLeuSerProAlaAspAlaLysProLe 44
DB 57 GAGGAAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 99
QY 44 ValGluLeuArgAlaAlaGlyLeuGluProValGlyLysIleGlyGluGluValGluThr 64
DB 100 -----CGGCTGTGGGAGCATATGAGAGAGGTGAGAGTGCAG 134
QY 64 rGluThrSerValAlaAsnValGlyProGluArgIleGlyProHisCysPheGluLeuLeu 84
DB 135 TGAGACACAGCGGTGAGCGTGGCCAGAGCCAGCATGCGGCCACTGTTGAGCTGCTGGCG 194
QY 84 gValLeuGlyLysGlyGlyGlyGlyGlyValPheGlnValArgLysValGlnGlyThrAs 104
DB 195 TGTGCTGGGCAAGGGGCGCTATGTGCAAGGTGTTCAGAGTGCAGAGGTCGACACCA 254
QY 104 pLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
DB 255 CTGGGCGAAATATATGCCATGAAAGTCCTAAGAGAGGCCAAATATGTGGCAATGCCAA 314
QY 124 sAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheI 144
DB 315 GGACACAGCAGACACACAGCGGCTGAGCGAACAATTCATGAGTCAAGTCAAGCACCCTTTAT 374
QY 144 eValGluLeuAlaTyrAlaPheGlnThrGlyGlyLysLeuTyrLeuIleLeuGluLysLe 164
DB 375 TGTGGAACGTGGCTATGCTTCACAGCTGGTGGCAAACTCTACTCTTAAAGTGGCT 434
QY 164 uSerGlyGlyGluLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThrA 184
DB 435 CAGTGTGGGAGAGCTC-----TTCTGTGGAGAGATACG 467
QY 184 lAcysPheTyrLeuAlaGluIleThrLeuAlaLeuGlnHisLeuHisSerGlnGlyTle 204
DB 468 CCGCTTTCTACCTGCTGATGATCAGCTGAGCTGGGCGCATCTCCACTCCACAGGATCA 527
QY 204 leryThrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 224
DB 528 TCTACCGGGAGCTCAAGCCCGAGAACATCATGCTGACAGCCAGGCGCCACATCAAACTGA 587
QY 224 hAspPheGlyLeuCysLysGluSerIleHisGluAlaValAlaThrHisThrPheCysG 244
DB 588 CCGACTTTGGACTCTGCAAGAGATCAATCATGAGGCGCGGCTCATCTACACCTTGTGGC 647
```

Qy	244	LYTHRIIEGLIYURYMETALAIProGIunIleuValARgerSLyIhIsAsnARgAlaValA	264
Db	648	GCACCAATGTGAGTACATGCCCCCTGGAATTCCTGGTGGCAGTGGCCACAACCGGGCTGTGG	707
Qy	264	SPTRPTPSerLeuGLYAlaLeuMeCTYAspMetLeuThrGlySerProProPheThra	284
Db	708	ACTGGTGGAGCCTGGGGGCCCTGATGTAGCACATGCTCACTGGATCGCCGCTTTACCG	767
Qy	284	IaGIuAsnARgLYsLYsThImeAspLYsIleIleARgLYsLYsLeuAlaLeuProProT	304
Db	768	CAGAGAACCGGAAGAAAAACCATGGATAGATCATCAGGGGGCAAGCTGGAGCTGCCCCCT	827
Qy	304	YrLeuThrProAspAlaIARgAspLeuValLYsLYsPheLeuLYsARgAsnProSerGlnA	324
Db	828	ACCCACACCCCAAGATGCCCCGGGACCTTGCAAAAAAGTTTCTGAACAGGAATCCACCGAGC	887
Qy	324	rgIIeGLyGLyGLYProGLYAspAlAlaAspValGIlnARghIsPhePheARghISM	344
Db	888	GGATTTGGGGGTGGCCCAAGGGGATGCTGCTGATGTGCAGAGACATCCCTTTTCGGGCACA	947
Qy	344	eIAsnTRPAspAspLeuLeuAlaTRPARgValAspProProPheARgProCYsLeuGlnS	364
Db	948	TGAATGTGGAGCAACCTTCTGGCCGTGGCGTGGACCCCTTTCAGGCGCTGTGCAGT	1007
Qy	364	erGIuGLIuAspValSerGlnPheAspThrARgPheThrARgClnThrProValAspSer	384
Db	1008	CAGAGGAGGAGCAGTGAAGCCATTGTGAATACCGGCTTCACAGCGACAGCGCGGTGGACAGTGC	1067
Qy	384	roAspAspThrAlaLeuSerGlnSerAlaAsnGlnIaPheLeuGlyPheThrTYrValA	404
Db	1068	CTGTATGACACAGCCCTCAGCGAGAAGTCCACACAGGCGCTTCTGGGCTTCACATACGTGG	1127
Qy	404	IaProSerValIleuAspSerIleLYsGlnGlyPheSerPheGlnProLYsLeuARgSerP	424
Db	1128	CGCGCTGTCTCTGAGACAGATCAAGAGGGCTTCTCTCCACGCCCAAGCTGGCCTTAC	1187
Qy	424	roARgARgLeuAsnSerSerProARgValProValSerProLeuLYsPheSerProPheG	444
Db	1188	CCAGGCGCCCTCACACAGTAGCCCGCGGGTCCCGCTCAGCCCTCAAGTTCTCCCTTTTG	1247
Qy	444	IuGIyPheARgProSerProSerLeuProGlnProThrIuLeuProLeuProProLeuL	464
Db	1248	AGGGGTTTCGGCCCAAGCCCTGCGGAGCCACGAGGTACTCTACTCTCCACATCC	1307
Qy	464	euProProProProProSerThrThralaProLeuProIleARgProProSerGlyThrl	484
Db	1308	TGCCACCGCGCGCCCTTCACACACCGCCCTCTCCCACTCCCTGCCCTTAGGGACCA	1367
Qy	484	YsLYsSerLYsARgLYsARgLYsARgLYsARgLYsARgLYsARgLYsARgLYsARgLYs	495
Db	1368	AGAGTCCCAAGAGGGGCGTGGCGTCCAGGGGCGC	1402
RESULT 4			
AAx61282			
XX	ID	AAx61282 standard; cDNA; 1637 BP.	
XX	AC	AAx61282;	
XX	XX		
DT	29-JUL-1999	(first entry)	
XX	XX		
DE	Human signal peptide-containing protein encoding cDNA SEQ ID NO:10.		
XX	XX		
KW	Human; signal peptide-containing protein; SP; cell proliferation; cancer; neuronal disorder; immune response; detection; ss.		
XX	OS	Homo sapiens.	
XX	PN	MO924463-A2.	
XX	XX		
XX	XX	20-MAY-1999.	
XX	XX		
XX	XX		
XX	XX	04-NOV-1998; 98MO-US23578.	

PR	07-NOV-1997;	97US-0966316.
PA	(INCY-)	INCYTE PHARM INC.
XX		
PI	Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;	
XX		
XX	WPI: 1999-337694/28.	
DR		
XX		
XX		
XX		
PS	cdna clones encoding signal peptide-containing proteins	
XX		
XX	Claim 4; Page 75-76; 83pp; English.	
CC	The present sequence represents a human cDNA clone encoding a signal	
CC	peptide-containing protein (SP). SP proteins can be used to stimulate	
CC	cell proliferation or to treat or prevent cancer. SP antagonists are	
CC	also used to treat or prevent cancer, and also for treating or	
CC	preventing neuronal disorders or immune responses. Polynucleotide	
CC	sequences complementary to the SP-encoding polynucleotides are useful	
CC	for the detection of SP-encoding nucleic acid molecules in biological	
CC	samples.	
XX		
XX		
SO	Sequence 1637 BP; 342 A; 473 C; 463 G; 332 T; 27 other;	
	Alignment Scores:	
	Pred. No.:	5.53e-123
	Score:	1947.50
	Percent Similarity:	90.89%
	Best Local Similarity:	90.44%
	Query Match:	74.50%
	DB:	20
		Gaps: 4
US-09-762-258-2 (1-495) x AAX61282 (1-1637)		
QY	9	GIYALAGLYALALAMETALALAVAlPhEASPLEUASPLEUGLUTRNGLUGLYSer 28
DB	180	GGGGCGGGCGGGCCGATGGCGGGCGGTGTATTGGATTGGAGCGAGGGAAGCGAGC 239
QY	29	GIUGLUGLUGLUGLUPROGLILEUSeRProALAAsPALaCysProLEUALAGLLeuArg 48
DB	240	GAGGGCGAGGGCGAGCCAGACTCAGCCCCGGAGCGCATGTCCCTTGGCGAATTAGG 299
QY	49	ALaALaGLyLeuGLuProVALGLYHISTryGLUGLUGLUGLLeuLethrGLUThrSerVal 68
DB	300	GCACGTGGCCCTAAGACCCTGTGGGACACTATGAAGAGGGGAGCGAGCTGAGACACCGCTG 358
QY	69	ASnVALGLYPROGLUArgILLeGLYProHIScysPheGLILEuLeuArgVALLeuGLYlys 88
DB	360	AACGTGGCCCGAGAGCGGATGGGGCCCCACCTGTGGAGCTGGCTGGCGGAG 419
QY	89	GLYGLYTryGLYlysVALPheGLINVALRgLYsVALGLNGLYThrAsnLeuGLYlysIle 108
DB	420	GGGGGCTTATGGCAGAGGTITTCAGGTGGGGAAGGTGCAGGACACCAACTTGGCGAAATA 479
QY	109	TYrALaMeTLysVALLeuArgLYsALaLYsIleVALArgASnALaLYsASPThrAlaHIS 128
DB	480	TATGCCATGAAGATGCTTAAGGAAGGCCAAATTTGGCCATGTGCCAAGACACAGCAC 539
QY	129	ThrArgALaGLuArgASnIleLeuGLUSeRVALYsHISProPheIleVALGLLeuALA 148
DB	540	ACACGGCGGTGAGCGGACATCTAGAGTCACTGAAGCACCCCTTATTATGTGGAACGTGCC 599
QY	149	TYrALaPheGLINTHGLYGLYlysLeuTYrLeuILE-LeuGLYcysLeuSeRGLYGLYGL 166
DB	600	TATGGCTTTCGACACTGGGGGAACCTCACTCACTTGGATTTGGCTCGACAGTGGTGGCA 655
QY	168	lLeuPheThrHISLeuGLuArgGLUGLYLLePheLeuGLUAsPThrAlaCysPheTYrLE 188
DB	660	GCTTTCACGCACTGTGGAGCGAGAGGCGATTTCTCTGGAAATACGGGCTCTCTACCT 719
QY	188	VALAGLlLeThrLeuAlaLeuGLYHISLeuHISSerGLNGLYLeILETYrArgAsPLe 208
DB	720	GGCTAGAGTTCACGGTGGCGCTGGGCCATCTCCACGGGCAATCACTACCGGGAGCT 779

QY 208 uLysPProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLe 228
 DB 780 CAAGCCCGAGAACATCATCTCTCAGCAGCGCCACATCAACATGACGACTTGGACT 839
 QY 228 uCysLysGluSerIleHisGlnGlyAlaValThrHisThrPheCysGlyThrIleGly 248
 DB 840 CTGCAGAGAGTATCATCAGAGGGCCCGCTCATCATCCTTCTGGCGCCATTAGTA 899
 QY 248 rMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTrpPseLe 268
 DB 900 CATGGCCCTGAGATCTGGTGGCAGTGGCCCAACCGGGCTGTGAGCTGGAGACCT 939
 QY 268 uGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsnArg 288
 DB 960 GGGGGCCCTGATGTACGACATGCTCACTGGATGGCCCTTACCCGACGAGAACCGGAA 1019
 QY 288 sLysThrMetAlaPheLysIleLeuArgGlyLysLeuAlaLeuProProTyrLeuThrPro 308
 DB 1020 GAAGACCATGAGTAAATCATCATCAGGGCAAGCTGAGCTCCCTTACCTCATCCACAGA 1079
 QY 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGlyLys 328
 DB 1080 TGGCCGGGACCTTGTCAAAAAGTTTCTGAACGAGATCCACGACGAGATTGGGGGTGG 1139
 QY 328 yProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTrpAsp 348
 DB 1140 CCCAGGGGATGCTGCTGATGTGCAGACATCCCTTTTCCGGACATGATGATGGAGCA 1199
 QY 348 pLeuLeuAlaTrpArgValAspProPhe--ArgProCysLeuGlnSerGluGluAsp 368
 DB 1200 CTT-CTGGCCTGGCTGTGGANCCCCCTTTCAGGCCCTGTGCTGAGTCAAGAGACG 1258
 QY 368 aLysGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspPThrA 388
 DB 1259 --GAGAGTTTGATACCCCTTCACACGGAGAGCGCGGTGGACATCCGATGACACAG 1316
 QY 388 lLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaProSerVal 408
 DB 1317 C-CTCAGCAGAGTGCACACAGGCCCTTCTGGGTT-ACATAGAGGGCGC-TCGTTC 1373
 QY 408 euAspSerIleLysGlnGlyPheSerPheGlnProLysLeuArgSerProArgArgLeu 428
 DB 1374 TGGACAG-ATCAAGAGG---TTCTCTTTCAGCCCAAGT-----GGGTCAACCGAGGCTC 1423
 QY 428 snSerSerProArgValProValSerProLeuLysPheSerProPheGlnGlyPheArg 448
 DB 1424 AANATAGCCCCGGG---TCCGTAGGCC---TCAAGTTTTCCTTNNAGGTTGGGCCA 1477
 QY 448 roSerProSerLeuProGluProThr 456
 DB 1478 GCCACCTTNCNGCCACGAGTACT 1503
 RESULT 5
 ABL65827
 ID ABL65827 standard; DNA; 2346 BP.
 XX
 AC ABL65827;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:4164.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX

PF 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 (AVAL-) AVALON PHARM.
 PA Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 DR
 XX
 DR WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 PS
 PS Claim 1; SEQ ID 4164; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

CC Infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.

XX Sequence 2346 BP; 750 A; 453 C; 558 G; 585 T; 0 other;

Alignment Scores:

Pred. No.:	2,67e-109	Length:	2346
Score:	1748.00	Matches:	354
Percent Similarity:	73.45%	Conservative:	50
Best Local Similarity:	64.36%	Mismatches:	80
Query Match:	66.87%	Indels:	66
DB:	24	Gaps:	8

US-09-762-258-2 (1-495) x ABL65827 (1-2346)

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QY 1 MetAlaArgGlyArgArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATGAGGCGACGAGAGAGCGGGGCTTTTACCACGCCCGGACTTCGAGACAGGAA 87
QY 14 -----MetAlaAlaValPheAspLeuAspLeuGluThrGluGluGlySerGluGly 30
Db 88 GCTGAGGACATGCGAGAGAGTGTTCACATACCTCGACGACGACGAGAGAGCGGGCTCT 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu--LeuArgAla 49
Db 148 GAGGATGAGCTGAGAG-----GAGGGGGCTCAGTTAAATGAAAGCATGGACCAT 195
QY 50 AlaGlyLeuGluPro-----ValGlyHisTrpGluGluValGluLeuThrGlu 65
Db 196 GGGGAGGTGGACATATGAACTGGCGATGGACATGTGTGAGAAATTTGAAATCTCAGAA 255
QY 66 ThrSerValAsnValGlyProGluArgTrpGlyProHisCysPheGluLeuLeuArgVal 85
Db 256 ACTGTGTGGAACAGAGGCGCCGAAAAATCAGACCCAGATGTTTGTGACTTCTCGGTA 315
QY 86 LeuGlyGlyGlyGlyTrpGlyValPheGluValAlaArgGlyValGluGlyThrAsnLeu 105
Db 316 CTGTGTAAGGGGGCTATGAGAAAGGTTTTCAGTACGAAAGTAAAGTAAAGTAAAGTAA 375
QY 106 GlyGlySerIleTrpAlaMetLeuValLeuArgGlyAlaGlyIleValArgAsnAlaAsp 125
Db 376 GGGAAATATTTGGCTTACATGAGGTGCTTAAAGGCAATGATGATGATGATGATGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValIleHisProPheIleVal 145
Db 436 ACAGCTCTACAAAAGCAGAAACGGAATATCTGGAGGAGTAAAGCAATCCCTTCATGCTG 495
QY 146 GluLeuAlaTrpAlaPheGluThrGlyGlyLeuTrpLeuIleLeuGluCysLeuSer 165
Db 496 GATTAAATTTATGCTTTCAGACGCTGCGAAACCTACCTCAGATCTCAGT 555
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
Db 556 GGAGGAGAACTATTTATGCTAGTAAAGAGAGGAAATATTTATGGAACACCTCCCTGC 615
QY 186 PheTrpLeuAlaGluIleThrLeuAlaLeuGluHisIleSerGluGlyIleIleTrp 205
Db 616 TTTTACTTGGGAGAAATCTCATGCTTGGGCTTTTACATCAAAAGGGGATCTATCAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThrAsp 225
Db 676 AGAGACCTGAGAGCGGAGAAATATCATGCTTATATCCAGAGTCATGTAACATAACAC 735
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValIleHisThrPheCysGlyThr 245
Db 736 TTTTGACATCTCAAGAAATCTTATCATGATGACAGTACACACACATTTTGTGGAACA 795
QY 246 IleGluTrpMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTrp 265
Db 796 ATAGAAATCATGCGCCCTGAAATCTTGATGAGAACTGGCCCAATCGTGTGTGATGG 855
QY 266 TrpSerLeuGlyAlaLeuMetLysAspMetLeuThrGlySerProPheThrAlaGlu 285

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Db 856 TGGAGTTGGGAGCATTAATGATGACATGCTGACTGGAGCACCCTTACCTGGGGAG 915
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysIleAlaLeuProPheTrpLeu 305
Db 916 AATGAAAAGAAAACAAATTCACAAAATCTCAAAATGTAATCTCAATTCCTCCCTACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysAspAsnProSerGlnArgIle 325
Db 976 ACACAGAGAGCCAGATGCTGCTTAAAGCGCTGAAAGAAAGAAAGCGCTTCCTGCTCG 1035
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetLsn 345
Db 1036 GGAGCTGCTCGGGGAGCTGAGAGAGTCAAGCTCATTCATCTTATGACACATTAAC 1095
QY 346 TrpAspAspLeuLeuAlaTrpArgValAspProPheArgProCysLeuGlnSerGlu 365
Db 1096 TGGGAGAGACTTCTGCTCGAAAGGTGAGGCCCTTTAAACCTCTGTGCAATCTGAA 1155
QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
Db 1156 GAGGATGTAAGTCATTTGATTCACAGTTTACAGCTCAGACACCTGTCGAGCAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTrpValAlaPro 405
Db 1216 GACTCAACTCTCAGTGAAGAGTCCCAATCAGCTCTTCTGGGTTTACATATGTGCTCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerProArg 425
Db 1276 TCTGTACTTGAAGAGTGAAGAAAGTTTCTTTTGAACCAAAATCCGATCACCTCGA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db 1336 AGATTATTTGCGACGCCACGAAACCTGTGACCCAGTCAATTTTCTCTGGGATTTTC 1395
QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
Db 1396 TGGGGAAGAGTGTCTTCCGCCAGC-----ACAGCAAAATCTCAGACACCTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db 1444 GAATACCCAAATGGAACAAGTGGCATAGACAGATGATGATGATGATGATGATGATGAT 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db 1504 TCGGACACACTTCCATATGACAGACGCCAATCTGGGCCCATACAAAAACAAGCTTTCC 1563
QY 484 ----- 484
Db 1564 ATGATCTCCAAAGCGCCAGAGCAGCTCGGTATGATATATGACAGACAAATGCTTTAAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db 1624 GAATTTAAGGCMAAAAGGTGAGAGGAGA 1653

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RESULT 6

ID AAF21858 standard; DNA; 1197 BP.

XX AAF21858;

XX 27-MAR-2001 (first entry)

DE Human breast and ovarian cancer associated antigen gene SEQ ID 245.

Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
neurotropic; neurproteolative; antiviral; antiallergic; hepatotropic;
antidiabetic; antifungal; antiparasitic; cardiant; immune disorder;
antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
Addison's disease; allergy; autoimmune haemolytic anemia;
autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
cardiovascular disorder; wound healing; neurological disease; ds.

PA (NOVS) NOVARTIS AG.
XX Kozma S, Stewart M, Thomas G;
XX WPI: 1998-120783/11.
DR P-PSDB: AAM52294.
XX New Isolated Drosophila p70 S6 Kinase - is used to develop products
PT for studying the kinase signalling pathway and for modulating the
PT kinase activity
XX
PS Claim 3; Page 38-42; 47pp; English.
XX
CC This sequence encodes the Drosophila p70 S6 Kinase (p70S6) of the
CC invention. The products are used in the study of the p70 S6 kinase
CC enzyme. They can be used for defining the p70 S6 kinase signalling
CC pathway and to develop agents for modulating the kinase activity. The
CC products can also be used for the production of antibodies and for
CC detection.
XX
SQ Sequence 2556 BP; 717 A; 663 C; 643 G; 533 T; 0 other;

Alignment Scores:
Pred. No.: 2.03e-89 Length: 2556
Score: 1455.00 Matches: 309
Percent Similarity: 66.73% Conservative: 52
Best local Similarity: 57.12% Mismatches: 115
Query Match: 55.66% Indels: 65
DB: Gaps: 10

US-09-762-258-2 (1-495) x AAV19873 (1-2556)
QY 13 AlalmetaAlaVal-----PheasPlau-----Aspleu 23
DB 471 GCAATGGCGGAGCTGAGGATCCCGACGACTGTTGACCTGGAGCTGCACCGCTGGAA 530
QY 24 ThrGluglUGlySerGlUGlyUGlyUGlyPro-----GluleuSerProAlaSP 40
DB 531 CTGCGAGCGACGAAGGCCAGGACTCGACGACGACGAGATGACTGGACGACTTGC 590
QY 41 AlAcysProLeuAlaGluleuArgAlaAlaGlUGlyLeuGluproValAlaGlyHisTrGlUGlu 60
DB 591 CTGAAACCG-----GAATTGTGTATTAATCTGCACCAAGACACTGAGGCCGAGACCC 644
QY 61 ValGluleuThrUGlyThrSerValAsnValAlaGlyProGlUGlyIleGlyProHisCysPhe 80
DB 645 ATACGCTCTGCGAGAGCAATGTTATCCAGCTAAATCAAGCTGGACCCAGACTTT 704
QY 81 GluleuLeuArgValIleUGlyLysGlyLysTrGlyLysValPheGlUGlyAlaArgLysVal 100
DB 705 GAGCTCAAGAAAGTCTTGGCAAGCGGTTATGGCAAGTATTTTCAGGTGGCGCAAGACC 764
QY 101 GlnglyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
DB 765 GCTGGACACGAGTGTAAACAATATTTTCCATGAAGTGCTCAAAAAGGCAATCCATTGTG 824
QY 121 ArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLys 140
DB 825 ACCAATCAAAAGGACGACGCGACCGCGCGCGCAATATCACTCGAGGCACTCAAG 884
QY 141 HisProPheIleValGluleuAlaTyrAlaPheGlnThrGlyLysLeuTyrIleu 160
DB 885 CATCCCTCATAGTGGACTAGTTATGCTTCCAGACGACGAGAAACTATACCTTATA 944
QY 161 LeuGlUGlySerGlyGlyLysIleuPheThrHisLeuGluArgGluGlyIlePheLeu 180
DB 945 CTGGAATATCTCAGCGGTGGAGCTGTTCATGACATTTGGAGCGTGAGGCGCATCTTCTTA 1004
QY 181 GluAspThrAlaCysPheTyrIleuAlaGluIleThrIleuAlaLeuGlyHisIleuHisSer 200
DB 1005 GAGGATACCACTGCTTATCTTAAGCAAAATCTTGGCTTGGCCATTTACACAA 1064
QY 201 GlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHis 220

DB 1065 CTGGGCAATCATCTACCGGATCTGAAGCCGAGAACATCTCTCGATGCACAGGACAT 1124
QY 221 IleLysIleuThrAspPheGlyLeuCysLysGlySerIleHisGluGlyAlaValAlaThrHis 240
DB 1125 GTGAAGCTCAGCGACTTGGACTGTGCAAGGACACATCAAGAGGATTTTGCACCCAC 1184
QY 241 ThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsn 260
DB 1185 ACCTTCTGCGGACAAATGATGATGACCTGAAATTTTACCAAGAGTGGCCATGCG 1244
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DB 1245 AAAGAGATGACTGTGGTGGCTGAGCGGCTCATGTTGATGATGCTGCACAGAGTCCCA 1304
QY 281 ProPheThrAlaGluAsnArgLysTrpMetAspLysIleIleArgGlyLysLeuAla 300
DB 1305 CCTTCACCGCGGAAATTCGAAGAGACATCGAGACCATTCGTGAACCCAGGTCAT 1364
QY 301 LeuProTrpTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsn 320
DB 1365 CTGCCAGCCTACCTTCACACCGGAGAGGATCTGTGTGTCGCTGATGAAGCGGACG 1424
QY 321 ProSerGlnArgIleGlyLysIleProGlyAspAlaAlaAspValGlnArgHisProPhe 340
DB 1425 GAACCTCAGCGGCTTGGCAGCGGAGCCGAGATGGCGGCGGTTCGAATATACACCATTC 1484
QY 341 PheArgHisMetAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgPro 360
DB 1485 TTCAAACACGTCACTGGGACATGTGTCTGCGACAGCGCTCGAGCGGCTTAAACCGG 1544
QY 361 CysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrPro 380
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QY 381 ValAspSerProAspAspThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeuGlyPhe 400
DB 1605 GTGATTCCTCCGATGATGATCAACGCTTAAGCGAAAGGCCAATTAATTTCCAAAGTTTC 1664
QY 401 ThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLys 420
DB 1665 ACCTACGTTGCACCTCGTACTGAGGATATGATCATCG-----GCCAACCGGATGCCA 1718
QY 421 LeuArgSerProArgArg-LeuAsnSerSerProArgValProValSer----- 436
DB 1719 GCACGCTCCCGACGACGACTCCACGCGCAGCTGCCGAGACGACTTCGCGCTGCAGTTTC 1778
QY 437 -----ProLeuLysPheSerProPheGluGlyPhe----- 446
DB 1779 CCATGGGCCAATGTGGGCGCAATGGCGCTGCTGGCGCATGACGCGTCAATTCGACAGATC 1838
QY 447 -----ArgProSe 449
DB 1839 CGGAGTGTTCGACGAGCACCGCCCGCATCATGACAGATTTTGCSCCGCTGCATC 1898
QY 449 rProSerLeuProGluProThrGlu-----LeuPro-----LeuProBr 462
DB 1899 GCCGGCGCAGGACGAGATGATGACGTGCGAGGCTGCGCGATGCTTAAAGCTGGAGCG 1958
QY 462 OleuLeuProProProProSerThrAlaProLeuProIleArgPro----- 479
DB 1959 ATTGCTCCCAACCAACCAACCAATCCCGTCGCTGCGTGCAGCAACCCAGCAACTG 2018
QY 480 -----ProSerGlyThrLysLysSerLysArgGlyArgGlyArg 492
DB 2019 CATCAAGCTTCCTCTCCCTACCCCAAAAAAAAAAAAAAAAAAAAAAACAGCAAAAG 2078
QY 492 g 492
DB 2079 A 2079
RESULT 8
ABL16561

Db 511 TCCCAGTTGAGGCGAGCTGGCCTAGAGTGAAGGGTCTGTTGGGGAGGGGGAAT 570
OY 53 ----- 53
Db 571 GGAGTGGGAAGGGGAACTGGGAGCAGCTGGACCTTGTCTCATTAATCTCTGTGTCC 630
OY 54 ----- ProValGlyHisTyrGluIuValGluLeuThrGluuHisSerValAsnValGlyP 72
Db 631 GTAGGCTGTGGACACTATGAAGAGGTGAGCTGACTGAGACGACGGTAAGTGGCC 690
OY 72 TGGIuArgIleGlyProHisCysPheGluLeuLeuArgValIeuGlyLysGlyTyrG 92
Db 691 CAGACCGATCGGGCCCACTGTTGAGCTGTGCTGGGCAAGGGGGCTATG 750
OY 92 Llys----- 93
Db 751 GCAAGGTAGGGGGGGCGGCGACCCCTCTCTGGCCTCACAGCCTCCATCTGGAGGCA 810
OY 93 ----- 93
Db 811 AGGTTCTCAAAACAATTAGACTTGTGAATCAGCAGGGCCTCTATGGGATTCAAGGC 870
OY 93 ----- 93
Db 871 AGAAACATAAAGAGGGAAGGCCAAATCCTTCATCGACTGAAATCTTCACTGCC 930
OY 93 ----- 93
Db 931 CACCCTTGGCAGGGCCTAGGCCCTCTGATCCCAAGCCAGAGCTTCAGGGTGGCCTT 990
OY 94 ----- -ValPheGln 96
Db 991 TGAAGATAGGATGTGAGAGGGAAGTGTGATCCTGTCCTGCCCTACAGGTGTTCCAG 1050
OY 97 ValArgLysValGlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLys 116
Db 1051 GGGCAAGGTGCAGGACCACTTGGGCAAAATATATGCATGAAGTCTCTAAGGAAG 1110
OY 117 Ala----- 117
Db 1111 GT-GAGTCACTGTCAGCCAAAGAACTACTGTGTGGCTCCATTCCCAACATGCTGTACC 1169
OY 117 ----- 117
Db 1170 AGGTTTGGGAAGACAGCAGGGAACAACAGTGGAGAGATCCCTGACTTGGGTTGCT 1229
OY 117 ----- 117
Db 1230 GGTATATGTCTGTGTGTATGTATTTGTTCTTGCAGTAATCTCAATGGGGCAATTTG 1289
OY 117 ----- 117
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OY 117 ----- 117
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OY 117 ----- 117
Db 1410 CCTGTCTCCAGGTTCAAGGAACTTCGTGCTTAGACTCCGAGTAGCTGGATAC 1469
OY 117 ----- 117
Db 1470 AGGCGTTGCCACACACCAGCTAATTTTGTACTTTTGTAGAGTGGGGTTCCGC 1529
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OY 117 ----- 117
Db 1590 GAGCTGGGATTACAGGCAATGAGCACCGTCCCTAGCTTTTATTTTATTTGATGAGTTC 1649

OY 117 ----- 117
Db 1650 TTGCTTTGTTCCCACTGAGAGTGCATAGTGCATCTCTGTCTACATGCAACTCTGCC 1709
OY 117 ----- 117
Db 1710 TCCCGGTTCAAGTAATCTTACTCTCAGCCCTGTAGTAGTGGAGTACAGGCTGT 1769
OY 117 ----- 117
Db 1770 GGCACACACCTGGCTAATCTTGTATTTCTATTGTTACCTACTTAATTTGAGAGGA 1829
OY 117 ----- 117
Db 1830 GTCTCACTGTCACTCAGGCTGGAAGTGCAGTGTGCGATCTGGCTCACTGGCAACTTC 1889
OY 117 ----- 117
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OY 117 ----- 117
Db 2010 TCATGTGTGACAGCTGTGTCTGAACCTCCTGACCTCAGGCTATCCGCTACCTTGGCTTC 2069
OY 117 ----- 117
Db 2070 CCAAGTGTGGGATTACAGCATGAACACACCGTGCCTGAGTTTGTACTTTTA 2129
OY 117 ----- 117
Db 2130 GTGAGCAGGGTTTCACCATGTGTGCTGAGCTGTCTGAACCTCTGACTCAGGTAT 2189
OY 117 ----- 117
Db 2190 TCGCTGCTCAACCTCCCAAGTGTGGGATTACAGTGTATCCACTGCGCTGGCAT 2249
OY 117 ----- 117
Db 2250 GGCACATTTTGAATGTCAAGCAGAGGGAGTGTACTGSCACCGGTGGGTGAGA 2309
OY 117 ----- 117
Db 2310 CCAGGATGCTGTGAACATCCACAGATGCGCAGGCGACCTCCACAAAGAAATGAC 2369
OY 117 ----- 117
Db 2370 CTGGTCCAGGTGTCAGTAGTGTGCCAGGTTGAGAAACCTGTGTGTAGAGATTAACCCAT 2429
OY 117 ----- 117
Db 2430 CCCTGAAATGATGCTGGTGAACAGCAGACAGATATATGAGAAATACATGCAGTGACAG 2489
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Db 2490 AGGATGACAGTAAACAACAGATGATGTCTGAGAGCTGTGGTCCCCCATTTT 2549
OY 117 ----- 117
Db 2550 TTTTATTTTATTTTGTGAGATAGTGTCTGCTCTGTCAACCAAGGCTGAGTGAAGTGGC 2609
OY 117 ----- 117
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OY 117 ----- 117
Db 2670 CCTGAGCTGGGATTACAGCGGTGTACATCATACCAGCTAATTTTCTATTTTATAGTAG 2729

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Q	y	165	-----	165
D	b	3870	GACTAGAGGCTCTGAGGGGACAGTGGCTGGTCTCTCATCTGTCGCCACGTTCAACCAAGC	3925
Q	y	165	-----	165
D	b	3930	ACAGGGCCAGGCACCGAGTAGGCGTCSGTAGATGTTTGTGAATTGAAATTGAATCCGAC	3985
Q	y	165	-----	165
D	b	3990	GGCAGCTGTGTAGGCGACAGTAGGCGGGAAATTATGAGCCCTCTTCCCAAGAAAGAAAT	4045
Q	y	165	-----	165
D	b	4050	AAAGACTCAGAAACACAAAGGGGCTTGGACCCAGACAGTGGGCTGTGACGTGTTGTGT	4105
Q	y	166	-----GlyGlyLeuLeuPheThrHisLeuGluAlaArgGlyIlePheLeuGluAspThrAla	184
D	b	4110	GGCAGGTGGGCAAGGCTCTTTCACGACTGTGGAGCAGAGGAGCATCTTCTGGAAGATACGGC	4165
Q	y	184	a-----	184
D	b	4170	CTGGTGGGTGTTATTCCTCCGCTTTCCTGAGGCTGGCAGGTCCCTGTCTACTCCGGCT	4225
Q	y	185	-----CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeu	198
D	b	4230	TCACCCCTCTCTGTTTCTGTGCAGCTCTTACCTGGCTGAGATACAGGCTGGGCTGGGCTCATC	4285
Q	y	198	euHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerG	218
D	b	4290	TCCACTCCCAAGGACATCATCTTACCGGACCTCAAGCCCGAAGACATCATGCTCAGCAGCC	4345
Q	y	218	ln-----	218
D	b	4350	AGGGTGGCATGTGTGTAGCGGAGCTGACAGCGGGGTCTGCAATGTGTGGGAGGGCTG	4405
Q	y	219	-----GlyH 220	220
D	b	4410	AGGACCTCTGTGGGTGGGGTGGGGCCCTGGTCACGCGCTCTCAACACCCCTCTCAGAGCC	4465
Q	y	220	IsIleLeuLeuThrAspPheGlyLeuCysLysGluSerIleHisGluAlaIleValIleThrH	240
D	b	4470	ACATCAAACTGACCGGACTTTTGAGATCTGCAAGGAGTCTATCCATGAGGGCGGCTGACTGC	4525
Q	y	240	IsThrPheCysGlyThrIleGluTyrMetAla-----	250
D	b	4530	ACACCTTCTGGCGGACCATTTGAGTACATGTGA - AGTGGACCTGTGCTGCCAGGGGTGGG	4585
Q	y	251	-----Prog 252	252
D	b	4589	GAGGACAGCCCGAAAGGGGACAGGCGCTGACTGACAGATTCCACTCGACCCAGGCGCCCTTG	4645
Q	y	252	IuIleLeuValArgSerGlyHisAsnArgAlaValAspTyrPheSerLeuGlyAlaLeuM	272
D	b	4649	AGATTCTGTGTGCGCAGTGGCCACACACCGGGCTGTGACTGTGTGAGACCTGGGGGCCCTGA	4705
Q	y	272	eTyrAspMetLeuThrGlySer-----	279
D	b	4709	TGTACGACATCTCATGTAGATCGCAAGTCCAGCCCGGGGAGAGAGGGGCGAGGGGC	4765
Q	y	279	-----	279
D	b	4769	AGAGGTGGGAGTAGCCCCCTCTGGGGGCAAGGGCAGGGCCTGTGTGGAGGCCCAAGG	4825
Q	y	280	-----ProPheThrAlaGluAsnArgLysLysThrM	291
D	b	4829	CTTCTCTACTTATGATCATCTCTCAGCGGCCCTTTCACCGCAGAGAAACGGAAAGAAACCA	4885
Q	y	291	eTAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeuThrProAspAlaArgA	311

Db 4889 TGGATTAAGTATCATACAGGGGCAAGCTGGACCTGCCCCCTACTACCCACCCAGATGCCGGG 4948
QY 311 sPLeuValLysLys----- 315
Db 4949 ACCTTGTCAAAAAAGGTGGACGTCCCTTCTCTCTCTCCGGGGCCCTGGCCAGCATTTCTGC 5008
QY 315 ----- 315
Db 5009 ACGTGTCTGTAGTCTCTCTGGGCTGTGGGAAGCCAGGGCCACCCGGCCTGTGCAGTT 5068
QY 315 ----- 315
Db 5069 TGCCTCTGGGAATGAAGAGGCCCTCCTTGAAGTCAAGGATGAGCCAGGCTCAGC 5128
QY 315 ----- 315
Db 5129 CCTGTCAAGACAGCAGCTGCTGCCCTGGCCAGTCTTAGGCTGAGTCTTAACCAAGTGACA 5188
QY 315 ----- 315
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Db 5309 CCAGGAGCCTTGCAAAAGCCTTTGTGAGAGAGTGCTCATTGACCAAACCTTGAAAGC 5368
QY 315 ----- 315
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QY 315 ----- 315
Db 5429 CCTACTCCAGCTAGCCCTGGAGCCGGGAGACATGACAGTACTTGGCCAGCCCTCA 5488
QY 316 ----- 315
Db 5489 CCCTCTCTCTGTGTCCTCCGAGTTTCTGAAACGGAAATCCACGAGGGGATGGGGTGGC 5548
QY 329 ProGlyAspAlaLysPyl----- 335
Db 5549 CCAGGGGATGTGTCGATGT -GCAGGTGGGTTTGGGACCAACACAGGGGTAGGGCTGAG 5607
QY 335 ----- 335
Db 5608 TCTCCAAAGGTGCCGGGAATGGGGGAGGGCCCAAGGCAGAGGAGTGCACGGGGGCA 5667
QY 336 ----- 341
Db 5668 ACCAGGGTAGCTGTAGTGGGTTTGGTCAATTTCTACTTACAGAGACATCTCCCTTTTTC 5727
QY 342 ArgHisMetAsnTTPAspAspLeuAlaTTPArgValAspProPheArgProCys 361
Db 5728 CGGACATGAATTTGGAGACACCTTCTGCGCTGGCGTGTGACCCCTTTCAGGGCCCTGT 5787
QY 362 Leu----- 362
Db 5788 CT -GGTGACAGCAGGGCTGTGTGCCAGTGTGCCGTGGCGGTGCAAGTGAAGAACTTG 5846
QY 363 ----- 367
Db 5847 CATCTGTGGTCCCTTGACCCCTCCCTCACTGTGGTGGCCACAGAGTGCAGAGGAGAC 5906
QY 368 ValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThr 387
Db 5907 GTGAGCACTTTGATACCGGCTTCAACAGGCAAGCCGGTGCAGTCTGTATGACACA 5966
QY 388 AlaLeuSerGlnSerAlaAsnGlnAlaPheLeu----- 398
Db 5967 GCCCTCAGGAGAGTGCACCAACAGGCCCTTCTGTGAGTGTGGGGGCTGTAGGCTGTGTG 6026

QY 398 ----- 398
Db 6027 GACACAGGACGAGATGCTACTAAGATGGACGACACTGAGTCTGCATGGCCCTGC 6086
QY 399 -----GlyPheThrTyValAlaProSerValLeuAspSerIleLysGlnLysPhe 415
Db 6087 CGCCCCCAGGCGCTTCACTATAGCTGGCGCGTCTGTCTGAGACAGCATCAAGAGGGGCTT 6146
QY 415 eSerPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVa 435
Db 6147 CTCCTTCAAGCCCAAGCTCGCTCACCAGGCGCTCAACAGTAGCCCGCGGCCCTGT 6206
QY 435 1----- 435
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QY 435 ----- 435
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QY 435 ----- 435
Db 6327 TCTATCATGGGAGCTCAGTTCCTTACACCCCTTGTGGCAGGCTGCTGGATGGAGTTT 6386
QY 435 ----- 435
Db 6387 GTTGAGCCCGCGGCTGTGTGCTGGGCAAGTGGGAAGGCTGCTTCCCTGACTGATG 6446
QY 436 -----SerPr 437
Db 6447 CTGGGAGCCTTGGGAGGCGCTAGAGGCTTATTCTGCTTGTTCCTTCCCTGCAGGCC 6506
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Db 6507 CCTCAAGTCTCTCCCTTTGAGGGGTTTGGCCACGCCACCCAGCCTGCCGAGGCCACGGA 6566
QY 457 uLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuProI 477
Db 6567 GCTACTCTTACTCCACTCTGTCACCGCCGCCGCCCTTGACACACGGCCCTTCCCAT 6626
QY 477 eArgProProSerGlyThrLysLysSerLysArgLysArgLysArgProGlyArg 495
Db 6627 CCGTCCCGCCCTCAGGAGCAAGAAATCCAAAGAGGGCCGTCGTCAGGGGCGC 6681
RESULT 12
AAK86891
ID AAK86891 standard; DNA; 4357 BP.
XX
AC AAK86891;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41703.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 07-JUN-2000; 2000US-0209467.
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PR 30-AUG-2000; 2000US-0227009.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236882.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 41703; 3071pp + Sequence Listing; English.
XX
CC AA654951 to AA64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AA682170 to AA691921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and

Oy	262	lAvlAsPTpTPrSeTleuGlYAlAleuMeTyrAspMeTleuThrGlySer	279
Db	2113	CTGTGGACTGGTGGAGGCTTGGGGGCTGTATGTACACATGCTCACTGGATCGCAAGTC	21727
Oy	279	-----	279
Db	2173	CAGCCCCGGGGAGAGAGAGGGGCAAGGGGCAAGAGGAGTGGAGTACCCCCCTCTGGGGGA	22323
Oy	280	-----	281
Db	2233	AGGGCGGGGCTGTGTGGAGGCCACAAAGGCTCTCTCACTTCCCTCTCCAGCGCG	2292
Oy	281	roPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaL	301
Db	2293	CTTTCACCGCAGAAACCGGAAGAAACCTGGATGAATCATCAAGGGGCAAGCTGGCAC	23525
Oy	301	eupProTyTLeuthrProAspAlaArgAspLeuValLysLys	315
Db	2353	TGCCCCCTACCTACCCCAAGATGGCCGGGACCTTGTCAAAAAGGTGCAGCTCCTTCTC	24121
Oy	315	-----	315
Db	2413	TCTTCTCCGGGGCCCTGCAGACCATTTCTGCAGCTGTTCCTGAATCTCTGGGCTGTGGG	24727
Oy	315	-----	315
Db	2473	GAAAGCCAGGGCCATCCGGGCTGTGCAGTTTGCTCTGGGAATGAAGAAGGCCCTCCCT	25323
Oy	315	-----	315
Db	2533	TGAAGTCAGGATTTGAGCCCAAGGTCTCAGCCCTGTACACAGACCAAGCTGCTGCCCTGGCC	25929
Oy	315	-----	315
Db	2593	AGTCCTTAGCGCTGAGTCCCTAAACAGTGCACAGCTGTGTGATGAGCTGGCCACACTTCCGTC	26525
Oy	315	-----	315
Db	2653	AAAGCGAGCATCGAGGTGTAGGGGGAGCGCGAGCACACATGGGGAGTTGGCGCT	27121
Oy	315	-----	315
Db	2713	CACCAAGCGCCCTTGGGGCAATGCCAGGGCCCAAGAGCTCTGCAGAAAGCTTTGTGGAGA	27727
Oy	315	-----	315
Db	2773	AGGTGCTCTCATGTGACCAAACTTGAAAGGCGCTGAGGATCATCATAGTGGGAGCCACAC	28323
Oy	315	-----	315
Db	2833	CCAAAAGCATTTCTCCCATGTCACTGACCCCTACTCCAGCTAGCCCTGGGAGCCGGGG	28929
Oy	316	-----	318
Db	2893	ACACATGAGCACTTGTGCCAGGCGCTCAACCTCTCTCTGTGCCGAGTTCTTGAAA	29525
Oy	319	ArgAsnProSerGlnArgGlyIleGlyGlyGlyProGlyAspAlaAlaAspVal	335
Db	2953	CGGAATCCCAAGCCAGCGGATTTGGGGGTGGCCCAAGGGGATGTCTCATGTGT -GCAGGTGGG	3011
Oy	335	-----	335
Db	3012	TTTGGGACCAACCAAGGGGTAGGGCTGAGTCTCAAGGGGTGCCGGGAATGGGGGCAAGG	3071
Oy	335	-----	335
Db	3072	CCCCAGGGCAGAGGAGTGAACCGGGGGGCAAGAGGGGTGAGCTGTTAGTGGGCTTTGGGTGC	31332
Oy	336	-----	351
Db	3132	ATTCTCAACCTACAGAGAACATCCCTTTTTCGGGACATGATGATTTGGGACACACTTCTGGGC	31939
Oy	352	TTPArgValAspProProPheArgProCysLeu	362

Db	3192	TTGGGGTGTGGACCCCCCTTTTCAGGGCCCTGTCT- GGTGACACACAGAGGCGTGGTGGCACTG	3250
Qy	362	-----	362
Db	3251	GCCGGTGGCGGTTGGCAAGTGGAGAACTGTCATCTTGTGCCCCCTGACCCCTCCCACT	3310
Qy	363	-----GlnSerGluGluAspValSerGlnPheAspThrArgPheThrArg	377
Db	3311	CTGTGGCGCCACACAGCATGTAGAGAGAGAGCTGTAGCCAGTTGTATACCGCTTCACAGG	3370
Qy	378	GlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPhe	397
Db	3371	CAGACGCCGGGTGGACAGTCTGTATGACACAGCCCTCAGCGAAGTGTCCACACAGGCTTC	3430
Qy	398	Leu 	398
Db	3431	CTGTGTAGTGGGGGGGCGCTCAGGCGCTGTGGGACACAGGACAGGATGTGTACTAAGATGG	3490
Qy	399	-----GlyPheThrTyrValAlaPrt	405
Db	3491	CAGGCACTGATGTGTGCATGTGCCCTCCACCCACCCCGAGGCGCTTCACATTAGTGGCGCC	3550
Qy	405	oSerValLeuAspSerLleLysGluGlyPheSerPheGlnProLysLeuArgSerProArg	425
Db	3551	GTCGTCTCTGGACAGCATCAAGAGAGGACTTCTCTTCACAGCCCAAGCTTGGCTCACCCAG	3610
Qy	425	gArgLeuAsnSerSerProArgValProVal 	435
Db	3611	GCGGCTCAACAGTACGTCGCCCGCGGGTCCCGCTCAGAGTACTGAGGAGAGTGGGGGTGTGTGC	3670
Qy	435	-----	435
Db	3671	TGGGTTAGGGAGCTGCGAGCGAGAGATGCCAGCTCCAGCCTTGGTGCTTGGCCACGTC	3730
Qy	435	-----	435
Db	3731	TGTGCGCCAGTGTGTGGCTTGTGGTGTCTGTGTCTATCATGTGGAGACTCACTCACTACACC	3790
Qy	435	-----	435
Db	3791	CTTGTGGCCACAGCGCTCGATATGGAGTTGTGTGAGACCCGGCGGCTGTGTGCTGGGAG	3850
Qy	435	-----	435
Db	3851	GTGGGAAAGGCTGCTCTCCCTGACTAGTGTCTGGAGCCCTGCGAGGCGCTAGAGAGCT	3910
Qy	436	-----SerProLeuLysPheSerProPheGluGlyPheArg	447
Db	3911	CTTATTCTGCTTGGTTTCCCTGTGCACGCCCCCTCAAGTTCTCCCTTTTGAAGGGTTTCG	3970
Qy	447	gProSerProSerLeuProGluProThrGlnLeuProLeuProProLeuLeuProProPr	467
Db	3971	GCCACGCCCCACGCTGTGGCGGAGGCCAAGAGGTACTTCACTCACTCACTCTCCACGCGC	4030
Qy	467	oProProSerThrThraAlaProLeuProIleArgProProSerGlyThrLysLysSerLys	487
Db	4031	GCCGCCCTCGACACGCCGCCCTCTCCCAATCCGTCCCTCCCTCAGGAGACCAAGAACTCCA	4090
Qy	487	sArgGlyArgGlyArgProGlyArg 495 	
Db	4091	GAGGAGCCGTGGCGCTCAAGGGCGC 4115	
RESULT 13			
AAH77989			
AAH77989 standard; DNA: 843 BP.			
AAH77989:			
xx	AC		
xx	DT	13-NOV-2001 (first entry)	
xx	xx		
xx	xx	Partial nucleotide sequence of human protein kinase SGK216.	

KM Human; protein kinase; cancer; immune disease; cardiovascular disease;
 KM brain disease; neuronal disease; Alzheimer's disease; chromosome 17;
 KM Parkinson's disease; multiple sclerosis; metabolic disorder;
 KM peripheral nervous system disease; amyotrophic lateral sclerosis;
 KM infection; ocular disease; migraine; pain; sexual dysfunction;
 KM mood disorder; attention disorder; cognition disorder; hypotension;
 KM hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
 XX Homo sapiens.
 OS
 FN WO200166594-A2.
 PD 13-SEP-2001.
 PF 02-MAR-2001; 2001WO-US06838.
 PR 06-MAR-2000; 2000US-0187150.
 PR 29-MAR-2000; 2000US-0193404.
 PR 13-NOV-2000; 2000US-0247013.
 XX
 XX (SUGE-) SUGEN INC.
 PA
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R,
 XX
 DR WPI; 2001-536777/59.
 XX P-PSDB; AAG67390.
 DR
 PT Nucleic acids capable of encoding human polypeptides having a kinase or
 PT kinase-like activity, useful for diagnosing a disease selected from
 PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
 XX Alzheimer's disease) -
 XX
 PS Example 1: Fig 1A; 201pp; English.
 XX
 CC The present sequence encodes a partial human protein kinase. The
 CC gene is located at chromosomal position 17q21.2-q22. The kinase
 CC polypeptides are useful for diagnosing a disease or disorder
 CC selected from cancers (e.g. cancers of tissues and cancers of
 CC hematopoietic origin), immune-related diseases and disorders.
 CC cardiovascular disease, brain or neuronal-associated diseases (e.g.
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis),
 CC metabolic disorders, peripheral nervous system diseases, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC infections caused by bacteria, infections caused by fungi, ocular
 CC diseases, migraines, pain, sexual dysfunction, mood disorders,
 CC attention disorders, cognition disorders, hypotension, hypertension,
 CC psychotic disorders, dyskinesias, and organ transplant rejection.
 CC Kinase inhibitors are useful for treating diseases and disorders
 CC described above.
 XX
 SQ Sequence 843 BP; 268 A; 173 C; 187 G; 215 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 1,81e-73 Length: 843
 Score: 1211.50 Matches: 224
 Percent Similarity: 90.07% Conservative: 30
 Best Local Similarity: 79.43% Mismatches: 27
 Query Match: 46.35% Indels: 1
 DB: 22 Gaps: 1
 US-09-762-258-2 (1-495) x AAH77989 (1-843)
 QY 117 AAlaySllleValArgasnaAlaySaPrhrAlaHlStHrArGlaGluArgSnllleu 136
 DB 1 GCAAATGATAGTAAAGAAATGCTAAAGATACAGCTCAACAAAGCAATGATATTCTG 60
 QY 137 GluSerVallySHISProPhelIleValGluLeuAlaTyrAlaPhelInHrglyGlyLys 156
 DB 61 GAGGAAGTAGAGGCATCCCTTCATGTGATTTAACTTAAGCCTTCAGACTGTGAAAA 120
 QY 157 LeuTyrLeuIleLeuGluCysLeuSerGlyGlyGluLeuPhenHrHISleuGluArgGlu 176
 DB 121 CTCTACCTCATCTCTGAGTATCTCAGTGGAGGAGAACCTATTATGACATTAGAAAGAG 180

QY 177 GlyIlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrleuAlaLeuGly 196
 DB 181 GGAAATTTTATGGAAGACACTCCCTCTTTTACTTGCGCAAAATCTCCATGGCTTTGGCA 240
 QY 197 HlSeuHlSSerGInglyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 216
 DB 241 CATTTACATCAAAAGGGGATCATATACAGACCTGAAAGCCGAGAGAAATTCATTCTTAAT 300
 QY 217 SerGInglyHlSllleLysLeuThrAspPheGlyLeuCysLysGluSerIleHISgluGly 236
 DB 301 CACCAAGGCTCATGTGAATTAACAGACTTGGACCTACAGCAAGAAATCTATTATATATGCA 360
 QY 237 AlaValIThrHISThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArg 256
 DB 361 ACAGTCACACACATTTTGTGAAACATAGATATCATGTGCCCCCTGAAATCTTGATGACA 420
 QY 257 SerGlyHlSAsnArgAlaValAspTyrPISerLeuGlyAlaLeuMetTyrAspMetLeu 276
 DB 421 ACTGGCCACAAATCGTGTGTGATTTGGAGATTGGGAGCATTTATGTATGACATGCTG 480
 QY 277 ThrGlySerProProPheThrAlaGluAsnArgLysLysThMetAspLysIleIleArg 296
 DB 481 ACTGGAGCACCCCATTTACTGGGGAATAGAAAGAAAACATTCACAAACATCCTCANA 540
 QY 297 GlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPhe 316
 DB 541 TGTAACTCAATTTGGCTCTCCCTACCTCACACAAAGAGCCAGATCTGTTAAAAGCTG 600
 QY 317 LeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGln 336
 DB 601 CTGAAAGAAATAGCTGCTCTCT--CTGGAGCTGGTCTCTGGGAGCGCTGAGAAAGTTCAA 657
 QY 337 ArgHISProPhePheArgHISMetLsnTrpAspAspLeuLeuAlaTrpArgValAspPro 356
 DB 658 GCTCATCTCATTCTTTAGACACATTAACCTGGAAAGAACTTCTGCTCAAAAGGTGGAGCCC 717
 QY 357 PropheArgProCysLeuInSerGluGluAspValSerGlnPheAspThrArgPheThr 376
 DB 718 CCTTTAAACCTCTGTGCAATCTGAAGAGATGTAAAGTATTCATTCCTCAAGTTTACA 777
 QY 377 ArgGlnThrProValAspSerProAspThrAlaLeuSerGluSerAlaAsnGlnAla 396
 DB 778 CGTCAGACACCTGTGACAGCCAGCATGACGCAACTCTCAGTGAAGTCCCAATCGAGTGC 837
 QY 397 PheLeu 398
 DB 838 TTTCTG 843
 RESULT 14
 ID ABL16560 standard; DNA; 12396 BP.
 XX
 XX ABL16560;
 AC XX
 DT 26-MAR-2002 (first entry)
 XX XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1153.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; peridontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX Homo sapiens.
 XX MO200228999-A2.
 XX 11-Apr-2002.
 XX 03-Oct-2001; 2001WO-US30821.
 XX 03-Oct-2000; 2000US-237189P.
 XX (GENE-) GENE LOGIC INC.
 XX Beezer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX WPI; 2002-435328/46.
 XX
 XX Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 PS Claim 1; SEQ ID NO 379; 114pp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 3061 BP; 681 A; 872 C; 875 G; 633 T; 0 other;
 Alignment Scores:
 Pred. No.: 3-22e-56 Length: 3061
 Score: 966.00 Matches: 199
 Percent Similarity: 61.99% Conservative: 75
 Best Local Similarity: 45.02% Mismatches: 127
 Query Match: 36.95% Indels: 41

DB: 24 Gaps: 7
 US-09-762-258-2 (1-495) x ABR83808 (1-3061)
 QY 1 MetaIaArgGlyArgArgAlaArgGlyValaGlyAlaMetAlaAla-ValPheAspLe 20
 DB 34 CTGGGGGGGAGATGGCGCTCGCCACCTCAAGAGAGCGCTGGCGCTCATAGAGCTAGT 93
 QY 20 uAspLeuGIuRhgIuGIuGIuYserGIuGIuYserGIuGIuYserGIuGIuYserProAlaAs 40
 DB 94 GCCGCTGAGACCGGAGAAATGGA--CAGACCTCAGAGGGA----- 130
 QY 40 pAlaCysProLeuAlaGIuLeuArgAlaAlaGIuLeuGIuPro-----ValGIuYH1 57
 DB 131 -----GAGCTGGACTTCAAGCCGCTCCAGAGATGAGAGCGT 165
 QY 57 sTyGIuGIuValGIuLeuThrGIuThrSerValAsnValGIuProGIuArgIleGIuPr 77
 DB 166 CCTCAAGGAGATCTCCACAGCGAC--CAGCTCAAGGCTGGCTGTGAGAGGCTGATCC 222
 QY 77 CHsCysPheGIuLeuLeuArgValLeuGIuYserGIuYserGIuYserGIuYserValPheGIuVa 97
 DB 223 ATCCCATTTCCAGCTCTCAAGGTTCTGGCCAGGGATCTTTGGCAAAATCTTCTGT 282
 QY 97 lArgIysValGIuGIuThrAsnLeuGIuYsIleTyAlaMetIysValLeuArgIysAl 117
 DB 283 GCGGAAGTCAACCGCGCTGACAGTGGGACCTGATGCTATGAGAGTGTCTCAAGAGGC 342
 QY 117 aLysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGIuArgAsnIleLeuGI 137
 DB 343 AAGCGTG-----AAAGTACGAGACCGCGCTCGGACCAAGATGAGAGAGACATCTGGC 396
 QY 137 uSerAlIysHisProPheIleValGIuLeuAlaTyAlaPheGIuThrGIuYsIle 157
 DB 397 TGATTAATCAACCCATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 456
 QY 157 uTyRleuIleuGIuGIuYsIleuSerGIuGIuLeuPheThrHisLeuGIuArgGIuGI 177
 DB 457 CTATCTCATCTGGACTCTCTCGGTGGGAGACCTCTTACCGCGCTCTCAAAAGAGT 516
 QY 177 yLlePheLeuGIuAspThrAlaCysPheTyRleuAlaGIuIleThrLeuAlaLeuGIuYH1 197
 DB 517 GATGTTACAGGAGAGAGATGTGAATTTTACCTGCGCAGCTGCGCTGCGGCTGATCA 576
 QY 197 sLeuHisSerGIuGIuIleTyRArgAspLeuYsProGIuAsnIleMetLeuSerSe 217
 DB 577 CCTGACAGCGCTGATCATTTACAGAGACCTCAAGCCTGAGACATCTCTGATGA 636
 QY 217 rGIuGIuHisIleLysIleuThrAspPheGIuLeuYsIleGIuSerIleHisGIuGIuYH1 237
 DB 637 GAGGGCCACATCAACCTCACTGACTTGGCTGAGCAAAAGGCCATTTGACCCAGAGAA 696
 QY 237 aValThrHisThrPheCysGIuThrIleGIuThrMetAlaProGIuIleLeuValArgSe 257
 DB 697 GAAGGCTATCTCTTCTCGCGGACAGTGAGATATGCGCCCTGAGTGCATCAACGCCCA 756
 QY 257 rGIuHisAsnArgAlaValAspTyrTyrSerIleuGIuAlaLeuMetTyRAspMetLeuTh 277
 DB 757 GGGCCACACCCATATGCGAGTGGGTGCTCATGTGGGGGTGGATGTGGATGTGGATCTTCA 816
 QY 277 rGIuSerProPheProPheThrAlaGIuAsnArgIysIysThrMetAspIysIleIleArgGI 297
 DB 817 GGGCTCCCTGCGCTTCCAGAGGAGAGACCGGAGAGACCATGATGATTTCTAAGGC 876
 QY 297 yLysLeuAlaLeuProProTyRLeuThrProAspAlaArgAspLeuValLysIysPheLe 317
 DB 877 GAAGCTAGCATATGCCAGTTTCTGAGCAGTGAAGCCAGAGACCTCTTGGGGCGCTGT 936
 QY 317 uLysArgAsnProSerGIuArgIleGIuGIuYserProGIuAspAlaAlaAspValGIuArg 337
 DB 937 CAAGGAGATCTCTGCAACCGGCTGCGTCCGCTTATGAGTGGGAGAGAAATCAACGC 996
 QY 337 gHisProPhePheArgHisMetAsnTyrPAspAspLeuAlaTyrPArgValAspProPr 357

[illegible]

```

01      QY      385  AspaSPrrtAlalauSerGIuseRAlaaNGlnAlaPheLeuGlyPhetheRtyrAla 404
02      Db      1149 GATGACAGAGCCCTCACCAGAGTAGTGGCCAAACAGAGCCTTCCTGGCGTTCAACAAGCTGGGC 1208
03      QY      405  ProSeRVallEuaapSseRIleLySGluGlyPheSeRPheGlnProLYSLeuArGerSePro 424
04      Db      1209 CCGGTCTGTCCCTGGACACATCAAGAGAGGGCGTTCTCCCTTCACGCCCAAGCTGGCGCTCACCC 1268
05      QY      425  ArqAgtLeuaNsensSerProArGVaIProValSerProLeuLYspHeSeRProphGlu 444
06      Db      1269 AGGGCCCTCAACACTAGCCCCCGGGGTGCCGTAGGCCCTCAAGTTCGCCCTTTTGAG 1328
07      QY      445  GlyPheaRGProSeRPSeRleuProGUlProThrGluleuProLeuProRoLeuLeu 464
08      Db      1329 GGGTTTGGCCCCACGCCCCAGCGTACGGAGACCCACAGAGACTACTACTACCTCATCTCG 1388
09      QY      465  PRoPRoPRoPRoPRoSeRTnTrHAlAProLeuPrOllEAyRProSoSeRtLythrLYs 484
10      Db      1389 CCACGCCGCGCGCCCTGTGACCACCGGCCCTCTCCATCCGTCCGCCCTCCAGGAGCAAG 1448
11      QY      485  LySSeRLysARgGLyARGGLyARgProGLyARg 495
12      Db      1449 AAGTCCAAGAGGGGCCCTGGGCGTCCAGGGCGC 1481
13
14 RESULT 2
15 US-08-966-316-10
16 ; Sequence 10, Application US/08966316
17 ; Patent No. 5932445
18 ; GENERAL INFORMATION:
19 ; APPLICANT: Lal, Preetl
20 ; APPLICANT: Au-Young, Janice
21 ; APPLICANT: Reddy, Roopa
22 ; APPLICANT: Murry, Lynn E.
23 ; APPLICANT: Mathur, Preete
24 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
25 ; NUMBER OF SEQUENCES: 18
26 ; CORRESPONDENCE ADDRESS:
27 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
28 ; STREET: 3174 Porter Drive
29 ; CITY: Palo Alto
30 ; STATE: CA
31 ; COUNTRY: USA
32 ; ZIP: 94304
33 ; COMPUTER READABLE FORM:
34 ; MEDIUM TYPE: Diskette
35 ; COMPUTER: IBM Compatible
36 ; OPERATING SYSTEM: DOS
37 ; SOFTWARE: FastSeq for Windows Version 2.0
38 ; CURRENT APPLICATION DATA:
39 ; APPLICATION NUMBER: US/08/966,316
40 ; FILING DATE: Herewith
41 ; CLASSIFICATION: 435
42 ; PRIOR APPLICATION DATA:
43 ; APPLICATION NUMBER:
44 ; FILING DATE:
45 ; ATTORNEY/AGENT INFORMATION:
46 ; NAME: Billings, Lucy J.
47 ; REGISTRATION NUMBER: 36,749
48 ; REFERENCE/DOCKET NUMBER: PF-0424 US
49 ; TELECOMMUNICATION INFORMATION:
50 ; TELEPHONE: 650-855-0555
51 ; TELEFAX: 650-845-4166
52 ; TELEX:
53 ; INFORMATION FOR SEQ ID NO: 10:
54 ; SEQUENCE CHARACTERISTICS:
55 ; LENGTH: 1637 base pairs
56 ; TYPE: nucleic acid
57 ; STRANDEDNESS: single
58 ; TOPOLOGY: linear
59 ; IMMEDIATE SOURCE:
60 ; LIBRARY: SKINBIT01
61 ; CLONE: 1869688
62
63 US-08-966-316-10

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Alignment Scores:

Pred. No.:	2.28e-161	Length:	1637
Score:	1947.50	Matches:	407
Percent Similarity:	90.89%	Conservative:	2
Best Local Similarity:	90.44%	Mismatches:	34
Query Match:	74.50%	Indels:	13
	2	Gaps:	4

US-09-762-258-2 (1-495) x US-08-966-316-10 (1-1637)

```

Qy 9 G1yAlaG1yAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThrGluGluGlySer 28
Db 180 GGGGGCCGGCCGGCCATGGCGCGCGCTGTTGATTGATTGGAGACGAGAGAACGACAC 239
Qy 29 G1uG1yGluGluGluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArg 48
Db 240 GAGGGCGAGGGGCGACCGAGCTCAGCCCCCGGAGCGCATGTCCTCCCTGCCAGATTGAGG 299
Qy 49 AlaAlaG1yLeuGluProValG1yHisTyrGluGluValG1uLeuThrG1uThrSerVal 68
Db 300 GAGCTGGCCCTGAGACCTCTGTGGACACATGTGAAGAGGTGAGCTGACTGACACGACGTG 359
Qy 69 AsnValG1yProGluArgG1leG1yProHisCysPheGluLeuLeuArgValLeuGlyLys 88
Db 360 AACGTTGGCCCGACGACGATCGGGCCCCACCTGCTTGACCTGCTGCTGCTGGGCAAG 419
Qy 89 G1yG1yTyrG1yLysValPheGluValArgLysValGluGlyThrAsnLeuGlyLysIle 108
Db 420 GGGGGCTATGGCAAGGCTTCCAGGTGCGAAAGTGCCAAAGCGCACCAACTTGGGCAAAATA 479
Qy 109 TyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAlaHis 128
Db 480 TATGCGATGAAGTCTTAAGGAAGGCCAAATTTGCGCAATGCCAAGACACAGCACAC 539
Qy 129 ThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleValGluLeuAla 148
Db 540 ACACGGCGTGACGGGACATCTCAGAGTCAGGAAGCACACCCCTTATTTGGAGACGGCC 599
Qy 149 TyrAlaPheGluThrGlyGlyLysLeuTyrLeuIle-LeuGluCysLeuSerGlyGly 168
Db 600 TATGCGCTTCCACAGCTGGTGGCAACTCACTCACTCTGATTCCTCAGTGGTGGCA 659
Qy 168 uLeuPheThrHisLeuGluArgG1uG1yIlePheLeuGluAspThrAlaCysPheTyrIle 188
Db 660 GCTCTTCACGCACTCTGGAGCGAGAGGGCATCTTCTCGAAGATACGGCTTCTTACT 719
Qy 188 uAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleIleTyrArgAspLe 208
Db 720 GGCTGAGATCACGCTGGCCCTGGCCATCTCCACTCCAGGGCATCATCTACCGGAGCT 779
Qy 208 uLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThrAspPheGlyLe 228
Db 780 CAAGGCCGGAACATCATGCTCAGACGCCAGGCCACACAACTGACCGACTTTGGACT 839
Qy 228 uCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGluTyr 248
Db 840 CTGCAAGGAGTATTCATCAGAGGGCGCGCTCACTACACCTTCTGCGGACCATGTGAGTA 899
Qy 248 rMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTyrSerLe 268
Db 900 CATGGCCCTGAGATTTCTGTGCGCAGTGGCCAAACCGGGCTGTGGACTGTGGAGGCT 959
Qy 268 uGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsnArgLy 288
Db 960 GGGGGCCCTGATGATGAGCATGCTCACTGATCGCGCCCTTACCGCGAGAACCGGGA 1019
Qy 288 sLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeuThrProAs 308
Db 1020 GAAAAACCATGATGAATCATCAGGGGCAAGCTGGCACTGCCCTTACTTCACTCAACCCACA 1079
Qy 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGluArgIleGlyGly 328

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Db 1080 TGCCTGGACCTTGTCAAAAAGTTTCTGAACGGAATCCACGACGCGATTGGGGGTGG 1139
Qy 328 yProGlyAspAlaAlaAspValGluArgHisProPhePheArgHisMetAsnTyrAspAs 348
Db 1140 CCCAGGGGATGCTGCTGATGATGACAGACATCCCTTTTCCGACACATGAATTTGGAGCA 1199
Qy 348 pLeuAlaLysPheValAspProPhe-ArgProCysLeuGluSerGluGlyAspY 368
Db 1200 CTT-CTGGCTGCGCGTGGANCCCTTTCAGAGCGCTGTGCAAGTGCAGTGCAGAGAGACT 1258
Qy 368 aLysGluPheAspThrArgPheThrArgGluThrProValAspSerProAspAspThrA 388
Db 1259 --GACAGATTATACCCCTTCAACAGCGACAGCGCGGTGACAGATCCTGATGACACAG 1316
Qy 388 lLeuSerGluSerLysAlaAsnGluAlaPheLeuGlyPheThrTyrValAlaProSerVal 408
Db 1317 C-CTCAGCGAGATGCCAACAGAGCGCTTCTGGGTT-ACATTAAGTGGCGCG-TCGTGTC 1373
Qy 408 uAspSerIleLysGluGlyPheSerPheGluProLysLeuArgSerProArgArgLeuA 428
Db 1374 TGGACAG-ATCAAGAG---TTCTGTTTACGCCCAAGT-----GGGTCAACAGGGCTC 1423
Qy 428 snSerSerProArgValProValSerProLeuLysPheSerProPheGluGlyPheArgP 448
Db 1424 AANATAGCCCGCGG---TCCGTNAGCCCC---TCAAGTTTNCCTTTNAGGTTGCGCA 1477
Qy 448 roSerProSerLeuProGluProThr 456
Db 1478 GCCACCTTNCNGGCCAAGAGTACT 1503

RESULT 3
US-08-749-902-4
; Sequence 4, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-0555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

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CLONE: Consensus
US-08-749-902-4

Alignment Scores:
Pred. No.: 3,76e-112      Length: 1607
Score: 1385.50           Matches: 285
Percent Similarity: 70.65%      Conservative: 40
Best Local Similarity: 61.96%    Mismatches: 69
Query Match: 53.00%             Indels: 67
                                      Gaps: 10
                                      2

US-09-762-258-2 (1-495) x US-08-749-902-4 (1-1607)

QY 86 LeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThrAsnLeu 105
    |||||:::|||||:::|||||
Db 227 CTGGGGAGGGGCGCTCATGCGCCGAGTGCAGACCTGC-----ATTAACTGT 271
QY 106 -----GlyLysIleTyrAlaMetLysValLeuArg-----LysAla 117
    ::::|:::|:::|:::|:::|
Db 272 ATCACCAGCCAGGAGTACNCCGTCANANATCATGTGTTTTTNCAGGCCACATTCGGAGC 331
QY 118 LysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGlu 137
    ::::|:::|:::|:::|:::|
Db 332 AGGCTTTCAGGAGGAGTGCAGATGCTTACCAGTCCAGGACACAGAGAGCTCTTAGAG 391
QY 138 SerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeu 157
    ::::|:::|:::|:::|:::|
Db 392 CTGATGTAGTTC-----TTCCGAGGAGGAGACCGCTTC 424
QY 158 TyrIleuIleLeuGlyLysLeuSerGlyGlyLysLeuPheThrHisLeuGluArgGlyGly 177
    |||||:::|:::|:::|:::|
Db 425 TACCTGGTGTGAGAAAGATGGGGGAGGCTCCATCTGAGCCCATCCACAGCGCGG 484
QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrIleAlaLeuGlyHis 197
    |||||:::|:::|:::|:::|
Db 485 CACTTCACAGCAGCTGCAGAGCCAGCGTGTGTGCAGACGCGGCCACCGCTTGACTTT 544
QY 198 LeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSer 217
    |||||:::|:::|:::|:::|
Db 545 CTGCTAATCAAAAGGATCGCCACAGGAGGACCTTAAGCCGGAATCTCTGTGACAC 604
QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
    ::::|:::|:::|:::|:::|
Db 605 CCCAACCAAGCTTCCTCCCGTAGAGATCTGTGACTTCGACCTGGCGGACCGCATCAATC 664
QY 229 -----CysLysGluSerIleHisGluGlyAla-ValThrHisThrPheCysGlyThr 245
    |||||:::|:::|:::|:::|
Db 665 AAGCGGAGCTGCTCCCTAT-CTCCACCCGAGACTGCTCACTCG-----TCCGGCTC 717
QY 245 rIleGluTyrMetAlaProGluIle----- 253
    ::::|:::|:::|:::|:::|
Db 718 GCGGAGTACATGCCCCGCGAGTAGTGAGAGCCTTCAGCGAGGAGGCTAGCATCTACGA 777
QY 254 -----LeuValArgSerGlyHisAs 260
    ::::|:::|:::|:::|:::|
Db 778 CAAAGCGCTGCAGACTGTGAGACCTGGCGCTCATCTTGTATATCTTACTACAGCGCTACCC 837
QY 260 nArgAlaValAsp---TrpTrpSer-----LeuGlyAlaLeuMetTyrAspMetLe 276
    |||||:::|:::|:::|:::|
Db 838 GCCCTGTGGGGCGCGTGGGAGGAGCAGATGCGGCTGGACCGCTGATGTATGACATAGCT 897
QY 276 uThrGlySerProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleAr 296
    |||||:::|:::|:::|:::|
Db 898 CACTGGATCGCGCCCTTACCGCAGAGAAACCGGAAACCAATGATGAATCATCAG 957
QY 296 gGlyLysLeuAlaLeuProProTyrIleuThrProAspAlaArgAspLeuValLysLysPh 316
    |||||:::|:::|:::|:::|
Db 958 GGGCAAGCTGGCACTNCCCTTACCTACCCAGATGCCGGGAGCTTGTCAAAAAAGTT 1017
QY 316 eLeuLysArgAsnProSerGlnArgIleGlyGlyProGlyLysAlaAlaAspValG 336
    |||||:::|:::|:::|:::|
Db 1018 TCTGAAGGCAATCCACAGCAGCGATGGGGGCGCCAGGGGATGCTGCTGATGTGCA 1077

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QY 336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaTrpArgValAspTr 356
    |||||:::|:::|:::|:::|
Db 1078 GAGACATCCCTTTTCCGGACATGATTTGGAGACACTTCTGCGCGGTGTGGACCC 1137
QY 356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheTh 376
    |||||:::|:::|:::|:::|
Db 1138 CCCTTTAGGCGCTGTCTGACATCAGAGAGAGAGATGAGCAATTTGATATACCCGCTTAC 1197
QY 376 rArgGlnThrProValAspSerProAspThrAlaLeuSerGluSerAlaAsnGlnAl 396
    |||||:::|:::|:::|:::|
Db 1198 ACGGACAGCCCGGTGACAGTCTGATGACACAGCCCTCAGGAGAGTGTCCAAACGAGC 1257
QY 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPhe 416
    |||||:::|:::|:::|:::|
Db 1258 CTTCCTGGGCTTCACATACCTGCGCGCTCTGCTCTGACAGATCAAGAGAGGCTTCTC 1317
QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 436
    |||||:::|:::|:::|:::|
Db 1318 CTTCCAGCCCAAGCTGCGCTCACCCAGCGCCCTCACAGTACAGTACCCCGGCTCCGTCAG 1377
QY 436 rProLeuLysPheSerProPheGlnGlyPheArgProSerProSerLeuProGluProTh 456
    |||||:::|:::|:::|:::|
Db 1378 CCCCCTCAAGTTCTCCCTTTGAGGGGTTTCGCGCCAGCCAGCTGCGGAGGCCAC 1437
QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrThAlaProLeuPr 476
    |||||:::|:::|:::|:::|
Db 1438 GGAGCTACCTTACCTCCTCCTGCGCACCGCGCCGCTCCAGCACCCCTCTCTCCC 1497
QY 476 oIleArgProProSerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
    |||||:::|:::|:::|:::|
Db 1498 CATCCGTCGCCCTCAGAGGACCAAGAGTCCAAAGAGGGGCGTGGGCTCCAGGCGCT 1555

RESULT 4
US-09-031-295-1
; Sequence 1, Application us/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGER, Tobieng
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1335
; US-09-031-295-1

Alignment Scores:
Pred. No.: 3,51e-61 Length: 2370
Score: 806.50 Matches: 172
Percent Similarity: 61.34% Conservative: 66
Best Local Similarity: 44.33% Mismatches: 111
Query Match: 30.85% Indels: 39
Gaps: 12

US-09-762-258-2 (1-495) x US-09-031-295-1 (1-2370)

QY 33 GLUPROGILUEUSERPROALASPALACYSPPROLEUALAGLULEUARGLAIAAGLYLEU 52
Db 235 GAGCCTGAGCTTATGAAAGCCAAACCTTCTCT-----
QY 53 GLUPROVALGILYHISTYRGLUGLIVVALGILUEUTHRGILUHSERVALASNAVAGLYPRO 72
Db 268 ---CCACCAAGTCTTCTCAGCAA-----ATCAACCTTGCCG 303
QY 73 GLUARGILEGILPROHISCYS-----PHEGLULEUARGVALLEUGLYLS 88
Db 304 TCGTCC---AATCCCATGCTAAACCATCTGACTTTCACCTTCTTGAAGTATCGGAAG 360
QY 89 GLYGLYTYRGLYLSVALPHEGLINVALRG---LYSVALGINGLYTHASNUGLYLS 107
Db 361 GGCAGATTGGAAAGGCTTCTTACCAAGACACAGGCAAGAAAGTG-----408
QY 108 ILEYTHAMETLYSVALLEUARPLYSALALYSILVALARGASNALYSAPTHRALA 127
Db 409 TTCTATGACAGCAAAAGTTTACAGAAAGCAATCTGAAAAG---AAGAGGAGAG 465
QY 128 HISTHARGALAGLUARGASNILE---LEUGLUSERVALYSHSPROPHLEVALGLU 146
Db 466 CATATTATGTCGAGCGGAATGTTCTGTGAAGATGTGAAGACCCCTTCTGCGGCG 525
QY 147 LEUALATYRALPHEGLINLTHGLYGLYLSLEUITYRLEULEUGLUCLEUSERGLY 166
Db 526 CTTCACCTTCTTCCACAGCTGCTGACAAATTTGCTTGTCTGACTACATTATAGT 585
QY 167 GLYGLULEUPHETHRHSLEUGLUARGLUGLYLIEPHELEUGLUSAPTHRALACYSR 186
Db 586 GGAGAGTTGTTCTACCATCTCCAGGAGACGCTCTTCTGGAACACAGGCGCTGTTT 645
QY 187 TYRLEUALAGLUILETHRLEUALALEUGLYSHISLEUHSERGLINGLYLIELEYARG 206
Db 646 TATGCTGTGAATATGACAGAGCGCTTGCGGTACCTGCATCTCAACATCGTTATAGA 705
QY 207 ASPLEULYSPROGLUASNILEMETLEUSERSERGLINGLYSHISLEULEUTHRASR 226
Db 706 GACTTAAACACAGAAATATTTTCTAGATTTCACAGGACACATGTCTTACTGATTTC 765
QY 227 GLYLEUCYSLYSGUSERLIEHISGLULYLAVALTHRHSTHRPHECYSGLYTHRI 246
Db 766 GGACTCTGCAAGAGATTGAACACAAACACACACATCCACTTGTGCGACGCG 825
QY 247 GLUTYRMETALAPROGLIILELEUVALARGSERGLYHISASNARGALAVALSPTTRP 266
Db 826 GAGTATCTCGACACCTGAGTGTTCATAGACGCTTATGACAGACACTGTGACGTG 885
QY 267 SERLEUGLYLALEUMETTYRASPMETLEUTHRGILYSERPROPHETHRALAGLUASN 286
Db 886 TGCCGTGGAGCTGCTGTATGAGATGCTGATGCGCTGCGCCCTTTATAGCGGAAC 945
QY 287 ARGLYSTYTHMETASPLYSILELEARGGLYLSLEUALALEUPROPROTYRLEUTHR 306
Db 946 ACAAGCTGAATATGACGACAACTTCTGAAACAGCCTCTCCACCAATTAATTTACA 1005
QY 307 PROASPALAARGASPLEUVALYLSYPHEULYSARGASNPROSERGLINARGILEG 326

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Db 1006 AATTCGCAAGACACCTCTCTGAGGCGCTCTCGCAGAGACAGCAAAAGCGGCTC---1062
QY 327 GLYGLYPROGLYASPALALASPVALGINRGHISPROPHETHRARGHISMETASPTTRP 346
Db 1063 GGGGCCAAGATGATTCATGAGATGAAGATGAAGTCACTGCTCTTCTTATTAATCACTGG 1122
QY 347 ASPASPLEULEUALATRPARGVALASPPROPHETHRARGVALASPPROCYSLAUGLINSERGLUGLU 366
Db 1123 GATGATCTCATTAATAAGAAAGTTACTCCCTTTTAACCCAAATGTAGTGGGCCAAC 1182
QY 367 ASPVALSERGLINPHEASPTTHRARGPHETHRARGLINTRPROVAL-----381
Db 1183 GAGCTACGACACTTGACCCCGAGTTTACCGAAGAG---CTGTCCCAACTCATTCATGCG 1239
QY 382 ASPSERPROASPSR-----THRALALEUSERGLUSERALASGLINALEUHEU 398
Db 1240 AAGTCCCTGACAGCGCTCTGTCACAGCCAGCGTCAAGGAAGTGCAGGCTTTCCTA 1299
QY 399 GLYPHETHRYRVALALAPROSER 406
Db 1300 GGCCTTTCCTATGCGCCCTCCACG 1323

RESULT 5
US-08-712-709-6
; Sequence 6, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-712-709-6

Alignment Scores:
Pred. No.: 7.57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39

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DB: 2 Gaps: 12
US-09-762-258-2 (1-495) x US-08-712-709-6 (1-2311)
QY 33 GluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
DB 202 GAGCCTGAGCTTATGATGAGCAACCCCTTCCTC----- 234
QY 53 GluProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
DB 235 ---CCACCAGTCTCTTCAGCAA-----ATCAACCTTGCGCCG 270
QY 73 GluArgGlyLeuGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
DB 271 TCGTGC---AATGCTCATGCTAAACCATCTGACTTCCTTCATTCCTGAAAGATCGGAAG 327
QY 89 GlyGlyTyrGlyValLeuPheGlnValArg---LysValGlnGlyThrAsnLeuGlyLys 107
DB 328 GGCAGATTGTTGGAAAGTTCTCTAGCAAGACACAGCAAGCAAGAGAGTGT----- 375
QY 108 IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
DB 376 TTCTATGCACTCAAGTTTACAGAGAAAGCAATCTGAAAAAG---AAGAGAGAGAG 432
QY 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
DB 433 CATATTATGTCGAGCGAGATGTTCTGTGAAGATGTGAAGCACTTCCTGCTGCGGC 492
QY 147 LeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGlyLysLeuSerGly 166
DB 493 CTTCACCTCTCTCTTCAGAGTGTGACAAATGTGACTTCTCCTGACACTCAATTAAATGT 552
QY 167 GlyGluLeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThrAlaCysPhe 186
DB 553 GGAAGAGTTGTTCAACATCTCCAGAGGAAAGCGTCTCTGGAACACAGCGGCTTC 612
QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
DB 613 TATGCTGCTGAATATAGCCATGCTGCGCTACCTGATCAGACATCGTTTATAGA 672
QY 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
DB 673 GACTTAAACAGAGATATTTGCTAGATTTCACAGGACACATGCTGCTTACGACTTC 732
QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValAlaThrHisThrPheCysGlyThrIle 246
DB 733 GGAAGCTGCAAGAGGAAATGAAACACACAGCAACATCCACTCTGTCGACCGC 792
QY 247 GluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266
DB 793 GAGTATCTCCACCTGAGGTGCTTCATATACAGCCTTATGACAGACTGTGAGCTGTG 852
QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
DB 853 TGCCTGGAGACTGTCTGTATGAGATGCTGTATGCGCTGCGCTTTTATAGCGGAAC 912
QY 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeuThr 306
DB 913 ACAGCTGAATGTAGCAACATTTGACACAGCCTCTCAGCGTGAACCAATATATACA 972
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326
DB 973 AATTCGCAACACACCTCGGAGGCGCTCTCAGAAAGACAGCAAGCGGCTC--- 1029
QY 327 GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPheArgHisMetAspTrp 346
DB 1030 GGGGCCCAAGGATCTCATGAGATTAAAGATGTCATGCTTCCTTAATTAATACG 1089
QY 347 AspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLysGlnSerGluGlu 366
DB 1090 GATGATCTCTATTAATAAGAGATTACTCCCTTTTAACCAATAATGTAGTGGGCCAAC 1149
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381

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DB 1150 GACCTACGCGCATTGACCCCGAGTTTACCGAAGAG---CCTGCCCCCACTCATTTGCC 1206
QY 382 AspSerProAspAsp-----ThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeu 398
DB 1207 AAGTCCCTGACAGCGCTGCTGACAGCCAGCGTCACAGAGCTGCGGAGGCTTCTCTA 1266
QY 399 GlyPheThrTyrValAlaProSer 406
DB 1267 GGCCTTCTATGCGCTCCACAGC 1290

RESULT 6
US-09-111-444-6
; Sequence 6, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ. ID NO.: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-09-111-444-6

Alignment Scores:
Pred. No.: 7,57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 3 Gaps: 12

US-09-762-258-2 (1-495) x US-09-111-444-6 (1-2311)
QY 33 GluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
DB 202 GAGCCTGAGCTTATGATGAGCAACCCCTTCCTC----- 234
QY 53 GluProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72

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Db 235 ---CCACCAAGTCCTTCCAGCAA-----ATCAACCTTGCGCCG 270
Qy 73 GUAArgIleGlyProHIScys-----PheGluLeuLeuArgValLeuGlyLys 88
Db 271 TCGTCC---AATCCCTGATGCTAAACCATCTGACATTCTTCTGAAAGTATCGGAAG 327
Qy 89 GUGlyTyrgIlyLysValPheGluValArg---LysValGInGlyThrAsnLeuGlyLys 107
Db 328 GGCAGTTTGGAAAGGTTCTTCTAGCAAGACACAAGGACAGAGAAGT----- 375
Qy 108 IleTyralIleMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
Db 376 TTCTATGACATCAAAAGTTTTCAGAGAACAATCTCGAAAGA---AAGAGAGAGAG 432
Qy 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
Db 433 CATATTTATGTCGAGCGGAATGTTCTGTGAAGATGGAAGCAACCTTCTCGTGGCG 492
Qy 147 LeuAlaTyralPheGInThrGlyLysLeuTyrlleuIleuGluCysLeuSerGly 166
Db 493 CTTACATCTTCTTCCAGACTGCTGACAAATTGTACTTGTCTTAGACTACATTATGCT 552
Qy 167 GUGlyLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
Db 553 GGAGAGTTGTCTTACCATCTCCAGAGGACGCTGCTTCTGGAACACGCGGCTGCTCC 612
Qy 187 TyrlleuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGInGlyIleIleTyArg 206
Db 613 TATCTCTGCTGAAATAGCCAGTCCGTGGCTTACCTGCAATCTGACATCATGTTATAGA 672
Qy 207 AspleuLysProGluAsnIleMetLeuSerSerGInGlyHisIleLysLeuThrAspPhe 226
Db 673 GACTTAAACCGAGAAATATTTGCTAGATTACAGGACGACATGCTTCTTACCTGACTTC 732
Qy 227 GUGlyLeuLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
Db 733 GGACTGTCGACAGAGAACATTGAAACAACAACAACAACATCACCCTTGTGGCAGCGG 792
Qy 247 GluTyrlleuAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrTrp 266
Db 793 GAGTATCTCCGACCTGAGGCTCTTCATTAAGCAGCCTTATGACAGACCTGGACGCTGG 852
Qy 267 SerLeuGlyAlaLeuMetLysAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
Db 853 TGCCTGGAGGCTGTCTGTATGAGATGCTGTATGCGCTGCCCTTTTATAGCCGAAC 912
Qy 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrlleuThr 306
Db 913 ACAGCTGAATGTTAGACACATCTGCAACAAGCCTCCAGCTGAACCAAAATATTACA 972
Qy 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGInArgIleGly 326
Db 973 AATTCGCAAGACACCTCTCGAGGCGCTCTGCAAGAGCAGACAGCAACGCGCTC--- 1029
Qy 327 GUGlyLysProGluAspAlaAlaAspValGInArgHisProPheArgHisMetAspThr 346
Db 1030 GGGGCGCAAGATGACTTCATGAGATTAAGAGTCACTGTCTTCTCTTAATTAACTGG 1089
Qy 347 AspAspLeuLeuAlaTrpArgValAspProPheArgProCysLeuGInSerGluLys 366
Db 1090 GATGATTCATTAAATAGAAAGATTAATCTCCCTTTTAAACCAAAATGTAAGGGCCAAAC 1149
Qy 367 AspValSerGInPheAspThrArgPheThrArgGInThrProVal----- 381
Db 1150 GACCTTAGCGCACTTTGACCCGAGTTTACCGAAGAG---CCTGTCTCCCACTCCATTGGC 1206
Qy 382 AspSerProAspAsp-----ThrAlaLeuSerGInSerAlaAsnGInAlaPheLeu 398
Db 1207 AAGTCCCTTGACAGCGTCTCTGTCAACAGCCAGCGTCAAGAGAGCTGCCGAGGCTTCTCA 1266
Qy 399 GlyPheThrTyrlleuAlaProSer 406
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Db 1267 GCGTTTCTTCTATGCGCTCCACAG 1290
RESULT 7
US-09-541-228-6
; Sequence 6, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-541-228-6
Alignment Scores:
Pred. No.: 7.57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 4 Gaps: 12
US-09-762-258-2 (1-495) x US-09-541-228-6 (1-2311)
Qy 33 GUGProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleGlyLeu 52
Db 202 GAGCTGAGCTTAAATGAAGACCAACCTTCTCTCT----- 234
Qy 53 GUGProValGlyHisTyrgIleGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
Db 235 ---CCACCAAGTCTTCTTCAGCAA-----ATCAACCTTGCGCCG 270
Qy 73 GUAArgIleGlyProHIScys-----PheGluLeuLeuArgValLeuGlyLys 88
Db 271 TCGTCC---AATCCCTGATGCTAAACCATCTGACATTCTTCTGAAAGTATCGGAAG 327
Qy 89 GUGlyTyrgIlyLysValPheGluValArg---LysValGInGlyThrAsnLeuGlyLys 107
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Db 328 GGCAGTTTGGAAAGGCTTCTTAGCAGACACAGGCGAGAGAGTG----- 375
Qy 108 ILETYAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
Db 376 TTCTATGACGTCAAAAGTTTACAGAAAGCAATCTCGAAAAG---AAAGAGGAGAG 432
Qy 128 HIsThArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
Db 433 CATATTATGTCGAGCGAGGAATGTTCTGTGAAAGATGTGAAGACACCTTCTCGTGGCG 492
Qy 147 LeuAlaThrAlaPheGlnThrGlyGlyLysLeuThrLeuIleLeuGluCysLeuSerGly 166
Db 493 CTTCACCTCTCTTCCAGAGCTGCTGACAAATGTACTTGTCTTAGACTACATTAATAGGT 552
Qy 167 GlyLLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
Db 553 GGAAGAGTTGTTTACCATCTCCAGAGGAGAGCGTGGCTCTGGAACACCGGGCTCGTCC 612
Qy 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
Db 613 TATGCTGCTGAAATAGCAGAGCTGCTGGGCTTACCTGCATTCACCTGAACATCGTTTATAGA 672
Qy 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
Db 673 GACTTAAACAGAGAAATATTTGCTAGATTCAAGGAGACAAATGTCTTACTGACTTC 732
Qy 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
Db 733 GGACTCTGCAAGAGAAACATTTGAACAACAACAGCAACATCCACTCTGTGGACGCCG 792
Qy 247 GluTyrMetLysProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrPhe 266
Db 793 GAGTATCTCCACCTAGAGGCTTTCATTAAGCAGCTTATACAGAGCTGTGGCTGGTGG 852
Qy 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
Db 853 TGCTTGGAGACTCTCTTGTATGAGATGCTTATAGCCCTGCCCTTTTATAGCCGAAC 912
Qy 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeuThr 306
Db 913 ACAGCTGAATGTACGACAACTTTCGAACACAGCTCTCCAGTGAACCAAAATATTACA 972
Qy 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnAlaGlyIle 326
Db 973 AATTCCGCAAGACACTCTCCGAGGGCTCTCCAGAGAGACAGCAAGACGCGCTC--- 1029
Qy 327 GlyGlyProGluLysAlaAlaAspValGlnArgHisProPheArgHisMetAsnTyr 346
Db 1030 GGGGCCAAGATGACTTCATGAGAGATTAGAGTCATGCTTCTTCTTCTTAATTACTGG 1089
Qy 347 AspAspLeuLeuAlaThrArgValAspProProPheArgProCysLeuGlnSerGluGlu 366
Db 1090 GATGATCTCATTTATAGAAGATTACTCCCTTTTAAACCAATGTAGACTGGGCCAAC 1149
Qy 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
Db 1150 GACCTACGGCAGCTTGAACCCCGAGTTTACCAGAGAG---CCTGTCCCAATCCATTGGC 1206
Qy 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerLysAsnGlnAlaPheLeu 398
Db 1207 AAGTCCCCCTACAGCGCTCTCGTACAGCCAGCTCAAGAGAGCTGGCGAGGCTTTCCTA 1266
Qy 399 GlyPheThrTyrValAlaProSer 406
Db 1267 GGCTTTTCCATGCGCTGCCACG 1290

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; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Alignment Scores:
Pred. No.: 1,2e-60 Length: 1599
Score: 797.50 Matches: 168
Percent Similarity: 59.858 Conservative: 69
Best Local Similarity: 42.428 Mismatches: 130
Query Match: 30.514 Indels: 29
DB: Gaps: 8

US-09-762-258-2 (1-495) x US-09-256-465-1 (1-1599)
Qy 48 ArgAlaAlaGlyLeuGluProValGlyHis-----TyrGluGlu 60
Db 424 CGGGCCCAAGCGAGGAGCCCATGAGTACAGTGTGGCTCCCGCAGTACTCTCCACG 483
Qy 61 ValGluLeuThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysPhe 80
Db 484 ACTGAGAGATGGAGTGGGGGTGACAGAGCGAGGAGCTTAAAGTGAACATGATGACTTC 543
Qy 81 GluLeuLeuArgValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysVal 100
Db 544 GACTATCTCAAACTCTCTGCGAAGGAGACTTTGGCAAGTACTCTCGTGGCGGAG--- 600
Qy 101 GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
Db 601 -----AAGCCCACTGGCCCTACTAGCCCATGAAGATCTCGGAAAGAAAGTCAATCAT 654
Qy 121 ArgAsnAlaLysAsp---ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerVal 139
Db 655 -----GCCAAGATGAAGTGCCTCACACAGTACAGGAGCGGGCTCTCCAGAACAC 708
Qy 140 LysHisProPheIleValGlnLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeu 159
Db 709 AGGCACCCGTTCTCTCACTGCGTGAAGTATGCCCTCCAGACCCAGCAGCGCTGCTTT 768
Qy 160 IleLeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGlyIlePhe 179
Db 769 GTGATGAGATATGCCAAGCGGGGTGAGCTGTCTTCCACTGTCCCGGAGCGGTGTTC 828
Qy 180 LeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlnLysLeuHis 199
Db 829 ACAGAGAGAGCGGGCCCGGTTTATGGTGCAGAGATTGTCTGGCTCTTGAGTACTGGAC 888
Qy 200 SerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGly 219
Db 889 TCGCGGAGAGCTGTATACCGCGACATCAAGCTGGAAGAACTCATGCTGGCGAAGATGGG 948
Qy 220 HisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThr 239
Db 949 CACATCAAGATCACTGACTTTGGCTGTGCAAGAGGCGCATGAGTACGGGCGCCACCATG 1008
Qy 240 HisThrPheCysGlyThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHis 259
Db 1009 AAAACCTTGTGTGGAGCCCGGAGTACTGGCCCTGAGGTGTGGAGAGCAATGACTAT 1068
Qy 260 AsnArgAlaValAspTyrPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
Db 1069 GGGCGGGCGCTGAGTGTGGGGCTGGGTGTGATCATGACAGATGATGCGGGCCG 1128
Qy 280 ProProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeu 299

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RESULT 8
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Lex M. Cowser

```



```

QY      340  PhePheatrgHshketaNTTPaspasPleuLeuAlATrphYValAspProProbhearg 359
          |||||  :::::  |||  :::::  :::::  :::::  :::::  :::::  :::::
Db      1309  TTTCTTCCACACATCAACTGGCAGAGCTGTGCTCCAGAGAGAGAGCTCTCTCCACCTTCAAA 1368
          |||||  :::::  |||  :::::  :::::  :::::  :::::  :::::  :::::
QY      360  ProCysLeuGlnSerGluGluAspValSerGlnPheaspPThrAlaLeuSerGlnSerAlaasnGln 378
          |||  ::|  |||||  |||  |||||  |||||  |||||  |||||  |||||
Db      1369  CCTCAGCTCAGCTCCGAGGTCGACACAGAGTACTTGATGATGAAATTACCGCCCAAGTCC 1428
          |||||  :::::  |||  :::::  :::::  :::::  :::::  :::::  :::::
QY      379  -----ThrProValAspSerProaspPThrAlaLeuSerGlnSerAlaasnGln 395
          |||||  |||||  |||  |||||  |||||  |||||  |||||  |||||
Db      1429  ATCAACATCAACACCCCTGACCGCTATGACAGCGCTGGGCTTACTGAGAGTGGACACAGCGG 1488
          |||||  |||||  |||  |||||  |||||  |||||  |||||  |||||
QY      386  Ala---PheLeuGlyPheThrTYR-----ValAlaPro--- 405
          |||  |||||  :::::  |||  :::::  :::::  :::::  :::::  :::::
Db      1489  ACCCACTTCCCCCAGTCTCTCTACTCGCCAGCATCCGGAGTGAAGACATGCCCCACGCG 1548
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      406  -----SerValLeuAspSerIleLeuGlyGlyPheSerPheGlnPro 419
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1549  AGAGGACCCAGCTCGCTGCTGCATCACCCTGGGTGGTTTTCACCCCT 1596
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RESULT 10
US-07-688-352C-25
? Sequence 25, Application US/07688352C
? Patent No. 5527896
? GENERAL INFORMATION:
? APPLICANT: Wigler, Michael H.
? APPLICANT: Colicelli, John J.
? TITLE OF INVENTION: Cloning by Complementation and Related
? TITLE OF INVENTION: Processes
? NUMBER OF SEQUENCES: 57
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
? ADDRESSEE: Bicknell
? STREET: Two First National Plaza, 20 South Clark
? STREET: Street
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60603
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patencin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/688,352C
? FILING DATE: 19910419
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/511,715
? FILING DATE: 20-Apr-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Borun, Michael F.
? REGISTRATION NUMBER: 25447
? REFERENCE/DOCKET NUMBER: 27805/30197
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 346-5750
? TELEFAX: (312) 984-9740
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1276 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 2..504
? US-07-688-352C-25

Alignment Scores: 1.05e-60 Length: 1276
Pred. No.:

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Score:	796.50	Matches:	182
Percent Similarity:	64.14%	Conservative:	63
Best Local Similarity:	47.64%	Mismatches:	110
Query Match:	30.47%	Indels:	32
DB:	1	Gaps:	4
US-09-762-258-2 (1-495) x US-07-688-352C-25 (1-1276)			
QY	29 GIUGLGLUGLUGLProGLuLeuSerProALAAspAlaCysProLeuAlaGLuLeuArg	48	
DB	71 GAACCTATGGAGAGAGAGAGATTAAACCA-----	1000	
QY	49 AAlaAlaGLuLeuLProValGLyHisTyrGLuGLuValGLuLeuThrGLuThrSer--	67	
DB	101 -----CAACGTGAAGACAGTATCAAGAAATTCATC	136	
QY	68 -----ValAsnValGLyProGLuArgLLeGLyProHisCysPheGLuLeuLeuArg	84	
DB	137 ACACATCATGTAAAGAGAGACATGAAGAAAGCAGATCCCTCCAGTTGAACCTTTAAAA	106	
QY	85 ValLeuGLyLysGLyGLyTyrGLyLysValPheGLuValArgLysValGLyThrAsn	104	
DB	197 GATTATAGGCGAAGGATCATTTGGAAAGSTTTTCTTAGTTAAAAAATCTCAGGCTCGAT	256	
QY	105 LeuGLyLysLLeTyrAlaMetLysValLeuArgLysAlaLysLLeValArgAsnAlaLys	124	
DB	257 GCTAGCAGAGCTTATGCCATGAGGTATTTGAAGAAAGCCACACTG-----AAAGTTCGA	310	
QY	125 AspThrAlaHisThrArgAlaGLuArgAsnLLeLeuLysSerValLysHisProPheLLe	144	
DB	311 GACCCAGTTCCGACAAAATGCAACGTGATCTTTGGTAGAGTTAATCATCTTTTATT	370	
QY	145 ValGLuLeuAlaTyrAlaPheGLuThrGLyLysLysLeuTyrLeuLLeuGLuCysLeu	164	
DB	371 GTCAGATTCGATTATCT--TTTCAAACTAGAGGAAAGTTGTATCTTAT--TTGGATTTTCTC	428	
QY	165 SerGLyGLuLeuPheThrHisLeuGLuArgGLuGLyLLePheLeuGLuAspThrAla	184	
DB	429 AGCGAGAGAGATTTGTTTACACGGTATTCAAAGAGGTGATGTTCACAGAAAGATGTC	488	
QY	185 CysPheTyrLeuAlaGLuLLeThrLeuAlaLeuGLyHisLeuHisSerGLyLLeLLe	204	
DB	489 AAATTCCTACCTGGCGAACTTCGACTTCCTTAAACATCTACATACCTCGGGAATATT	548	
QY	205 TyrTAspPLeuLysProGLuAsnLLeMetLeuSerSerGLyHisLysLLeThr	224	
DB	549 TATTAAGACTTAAACCGAAATATCTCT--CTTATGACAGAGGTCACATCACTTACCA	607	
QY	225 AspPheGLyLeuCysLysGLuSerLLeHisGLuGLyAlaValThrHisThrPheCysGLy	244	
DB	608 GATTTCCGGCTTAAGTAAGAGCTATTAACCATGAAGAAAGCAATATCT--TTTGTGGA	666	
QY	245 ThrLLeGLyTyrMetAlaProGLuLLeLeuValArgSerGLyHisAsnAlaGlaValAsp	264	
DB	667 ACTGTGGAGTATATGCGTCCAGAAGTATGTATGTGTGAGAGTCTACTCAGAGTGTGAC	726	
QY	265 ThrPTrSerLeuGLyAlaLLeMetLysPheMetLeuThrHisLysPro--ProPheThrAl	284	
DB	727 TGGTGCTCTTTGGTGCTTATGTGTGAATAGCTTACTGTGTACCATCCCTTTCACAGG	786	
QY	284 gLusAsnArgLysLysThrMetAspLysLLeLLeArgGLy--LysLeuAlaLeuProPro	304	
DB	787 AAAAAGATCGAAAGAAACAAATGACTATGATTTCTTAAAGCCAAAACTTGGAAATGCCACAGT	846	
QY	304 yTrLLeThrProAspAlaLArgAspLeuValLysLysPheLeuLysArgAsnProSerGLu	324	
DB	847 TTTTGTAGTCTCGAAGCGCAGAGCTGTTTACAAAGAGCTTTTAAAGCGAAATCTGCACAAACA	906	
QY	324 rGLLLeGLyGLyProLysrAspAlaAlaSerValGLuArgHisProPheThrArgHisM	344	
DB	907 GATTATGGTGCAGAGCCACATGAGCTTGAAGAAATTTAAAGACATTCATTTTCTCAACGA	966	
QY	344 eLAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuHis	364	

Db 967 TAGACTGAAATTAACCTGATFAGAGA-GAAATTCATCCGCCATTTAAACCTCAACGGCA 1025
Qy 364 ergluGluaspValserGlnPheaspThrArgpHeThrArgGlnThrProValaspSerp 384
Db 1026 GGCCGTAGAGATACATCTTATTTTGTGCTGAGTTTACTGCAAAAAACCTCCCAAAATTCAC 1085
Qy 384 roaPaapThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyVala 404
Db 1086 CT---GGCATTCACCTAGTCTTAATGCATACAGCTTTTGGGGGGGTTTGTGTTG 1142
Qy 404 Ia 404
Db 1143 CT 1144
RESULT 11
PCT-US91-02714-24
Sequence 24, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Migler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..504
PCT-US91-02714-24
Alignment Scores:
Pred. No.: 1.05e-60 Length: 1276
Score: 796.50 Matches: 182
Percent Similarity: 64.14% Conservative: 63
Best Local Similarity: 47.64% Mismatches: 110
Query Match: 30.47% Indels: 32
Gaps: 4

US-09-762-258-2 (1-495) x PCT-US91-02714-24 (1-1276)
Qy 29 GluGluGluGluGluGluGluGluSerProAlaaspAlaCysProLeuAlaGluLeuArg 48
Db 71 GAACCTATGGAGAGAGAGAGATTAACCA----- 100
Qy 49 AlaIaGluLeuGluProValGlyHisIstGlyGluValGluLeuThrGluThrSer--- 67
Db 101 -----CAAACTGAAGAGCATATCAAAAGAAATTCGATC 136
Qy 68 -----ValAsnValGlyProGluArgIleGlyProHisCysPheGluLeuArg 84
Db 137 ACACATCATGTAAGAAGAGACATGAAGAAGCAGATCCTCCAGTTGAATTTAA 196
Qy 85 ValLeuGluGluGlyGlyGlyGlyValArgGlnValArgGlnValArgGlnValArgGln 104
Db 197 GTATTAGGCGAGGATCTTTGGAAAGGTTTCTTGAATAAATACTCAGGCTGAT 256
Qy 105 LeuGlyLysIleTyAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
Db 257 GCTAGGCGAGCTTTATGCCATGATGATGAAGAAGCCACAGT-----AAAGTTGCA 310
Qy 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
Db 311 GACCGAGTTCGACAAAATGAACGTGATCTTGAGAGATTAATCATCTTTAT 370
Qy 145 ValGluLeuAlaTyAlaPheGlnThrGlyGlyLysLeuTyLeuIleLeuGluCysLeu 164
Db 371 GTCAAGTTGCATTTATCT-TTTCAAACGTGAAGGAGGTTGATCTTAT-TTGGAATTTCTC 428
Qy 165 SerGlyGlyLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThrAla 184
Db 429 AGGCGAGAGATTTGTTTACACGCTTATCCAAAGAGATGATTCACGAAGAAGATGTC 488
Qy 185 CysPheTyLeuAlaGluIleThrLeuAlaLeuGlnHisLeuHisSerGlnGlyIleIle 204
Db 489 AAATTTCTACGTGGCTGAACCTGCACTTCTTAGACATCACTGAGCTGGATAT 548
Qy 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThr 224
Db 549 TATAGAGACTTAAACCGAAATATCTT-CTTGATGAAGAAGTCATCAATCAAGTTAACA 607
Qy 225 AspPheGlyLeuCysLysGluSerIleHisGluAlaValThrHisThrPheCysGly 244
Db 608 GATTTGCGCTTAAGTAAGAGATCTTATGACATGAAGAAGCATATCT-TTTTGTGCA 666
Qy 245 ThrIleGluTyMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAsp 264
Db 667 ACTGAGAGTATATGGCTCCAGAGTAGTAAATGCTGAGATCACTACAGAGCTGAC 726
Qy 265 TyrTrpSerLeuGlyAlaLeuMetLysTrpMetLeuThrGlySerPro-ProPheThrAl 284
Db 727 TGGTGGCTTTTGGTGTATATGTTGAATGCTTACTGTGATACCATCTCTTCCCAAG 786
Qy 284 agLAsnArgLysLysThrMetAspLysIleIleArgLysLysLeuAlaLeuProprot 304
Db 787 AAAAGATCAAAAGAAACAAATGACTATGATCTTAAACCAAACTTGGAATGCCACAGT 846
Qy 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGln 324
Db 847 TTTTGAGTCTGTAAGCGCAGAGCTTTTACGAATGCTTTMAAGCGAATGCTGCAAA 906
Qy 324 rglIleGlyGlyProGlyAspAlaIaaspValGlnArgHisProPheArgHisM 344
Db 907 GATTAGGTGACAGACACATGAGTGAAGAAATTAAGACATTCATTTTCCCAACGA 966
Qy 344 etAsnTrpAspAspLeuLeuAlaTrpArgValAspProPheArgProCysLeuGlns 364
Db 967 TAGACTGAAATTAACCTGATFAGAGA-GAAATTCATCCGCCATTTAAACCTCAACGGCA 1025
Qy 364 ergluGluaspValserGlnPheaspThrArgpHeThrArgGlnThrProValaspSerp 384
Db 1026 GGCCGTAGAGATACATCTTATTTTGTGCTGAGTTTACTGCAAAAAACCTCCCAAAATTCAC 1085

Alignment Scores:

Pred. No.:	1,066-57	length:	2610
Score:	767.50	Matches:	165
Percent Similarity:	58.72%	Conservative:	64
Best local Similarity:	42.31%	Mismatches:	131
Query Match:	29.36%	Indels:	30
DB:	3	Gaps:	7

US-09-762-258-2 (1-495) x US-09-091-058-1 (1-2610)

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Db	531	GAAGCAGAGAGAGAGAGATGACTCCGGCTCACCCAGTGCACACTACAGGGC	590
QY	44	uAlaGluLeuArgAlaAlaGluLeuGluProValGlyHisTyrGluGluValGluLeuTh	64
Db	591	TGAAGAGATG-----	600
QY	64	rgLubThSerValAsnValGlyProGluArgLLeGlyProHisTyrSPhneGluLeuLeuAr	84
Db	601	-GAGGTGTCCCTGGCCAAAGCCCAAGCAGCCGTGACCATGAAGACGATTGATGACTGTAA	659
QY	84	gValLeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGlnGlyThAs	104
Db	660	GCTGTGTGGCAAGGACACTTTCGGCAAGGTGATCCTGTGAAGAG-----AAGC	710
QY	104	nLeuGlyLysLLeTyrAlaMetLysValLeuArgLysAlaLysLLeValArgAsnAlaL	124
Db	711	CACAGCGCGGTACTACGSCCATGAAAGATCTCAAGAAAGATGATCGTG-----GCCAA	764
QY	124	sAsP---ThAlaHisThrArgAlaGluArgAsnLLeLeuGluSerValLysHisProPh	143
Db	765	GGAAGAGGTGGCCCAACACTACCCAGAAAGCCGCTCCGCAAGAACTCCAGCACCCCTT	824
QY	143	eLLeValGluLeuAlaTyrLysLLePheGlnThrGlyLysLysLLeuTyrLysLLeuGlyC	163
Db	825	CTTCACAGCCCTTAAGTACTCTTCCAGACCCACAGCAGCCCTGTGCTTGTATGAGATA	884
QY	163	sLeuSerGlyLysLLeuPheThrHisLLeuGluArgGluGlyLLePheLeuGluAsPTh	183
Db	885	CGCCAAAGGGGGAGAGTGTTCTTCCACTGTCGCCGGAAGCTGATGTTCTCCGAGACCG	944
QY	183	rAlaCysPheTyrLeuAlaGluLLePheThrLeuAlaLeuGlyHisLLeuHisSerGln---G	202
Db	945	GGCCCGCTTGTATGGCGCTGAGATGTTGTACAGCCCTGCAGTCACTGCACCTCGAGAA	1004
QY	202	yLLeTyrArgAsPLeuLysProGluAsnLLeMetLeuSerSerGlnGlyHisLLeu	222
Db	1005	CGTGTATTCCGGGACCTCAAGCTTGAGAACTCATAGCTGTGCAAGAGAGGGCCACTTAA	1064
QY	222	sLeuThrAsPPhGlyLeuLysLysGluSerLLeHisGlnGlyAlaValThHisThPh	242
Db	1065	GATCAACGACTTGGGGCTGTGCAGAGAGGGGATTCAAAGAGCGGTGCCACCATTAACACTT	1124
QY	242	eCysGlyThrLLeGluTyrMetAlaProGluLLeuValArgSerGlyHisAsnArgAl	262
Db	1125	TTTGGGACACACTGATAGTACTGGCCCCGAGGTGTGGAGACATGACTAGGCGCTGTC	1184
QY	262	aValAsPTrpTrpSerLLeuGlyLLeuMetLysPheMetLysPheLLeuThngLysProProPh	282
Db	1185	AGTGAATGTGTGGGGCTGGGCTGTGCATGACAGAGATGATCGGTGGCGCTGCCCTT	1244
QY	282	eThrAlaGluAsnArgLysLysThrMetAsPLeuLLeLLeArgGlyLysLLeuAlaLeuPr	302
Db	1245	CTAACACAGGACACATGAGAACTTTTACAGCTCATCTCATAGAGAGATCCGCTTCC	1304
QY	302	oProTyrLeuThProAsPAlaArgAsPLeuValLysLysPheLLeuLysArgAsnProSe	322
Db	1305	GCGCAGCCTTGTCGCCAGGCGCAAGTCCTTGCTTCAAGGCTGTGCACAAAGAGACCCCA	1364
QY	322	rgLnaArgLLeGlyGlyGlyProGlyLysPalaAlaAsPValGlnArgHisProPhePhAr	342
Db	1365	GCAAGAGCTTGGGGGGGCTCCGAGGACCAAGAGATGATCATGACGATTCGGCTTGGC	1424

QY	342	ghlsmEaSTnTTPAspAspleuEuaLlrrPrpAylaSPAsPrOpPhEaSPrOCysLe	362
Db	1425	CGGTATGTGTGGAGCAGCAGCTGTGCAGAGAGAAGAGCTCAAGCCCACTTCAMGCCCCAGGT	1484
QY	362	uGlnSerGlUGlUaSPyAlaSerInPheAsPThrArpPheThrArGln-----	378
Db	1485	CAGCTGGAGAGCTGCACACCAGTATTTTGTATGAGAGATTCAAGGGCCAGATGATCACCAT	1544
QY	379	-ThrProValaSPSerProAspAsPThrAlaUeSerGlUaSerAlaasnGlnAla---Ph	397
Db	1545	CACACACACCTGCAGCAGATATGCATGTGTGTGACACGCGAGCGCCCACTT	1604
QY	397	eUeUGlYpHeThrThYrValAlaProSer	406
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RESULT 14
US-08-474-379C-25
: Sequence 25, Application US/08474379C
: Patent No. 5977305
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: GENERAL INFORMATION:
: APPLICANT: Wiegler, Michael H.
: APPLICANT: Collicelli, John J.
: TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
: TITLE OF INVENTION: PROCESSES
: NUMBER OF SEQUENCES: 88
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive/6300 Sears Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,379C
: FILING DATE: 07-JUN-1995
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/511,715
: FILING DATE: 20-APR-1990
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/206,188
: FILING DATE: 01-MAR-1994
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/688,352
: FILING DATE: 19-APR-1991
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Clough, David W.
: REGISTRATION NUMBER: 36,107
: REFERENCE/DOCKET NUMBER: 27866/32771
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
:
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1273 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
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: MOLECULE TYPE: CDNA
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: FEATURE:
: NAME/KEY: CDS
: LOCATION: 2..502
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: US-08-474-379C-25
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: Alignment Scores:
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: Seq. ID: 1
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OY 49 AlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeuThrGluThrSer--- 67
DB 101 -----CAACCTGAAGAGATCGATCAAGAAATTCGAATC 136
OY 68 -----ValAsnValGlyProGluArgGlyLeuGlyProHisCysPheGluLeuLeuArg 84
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DB 197 GTATTAGGGCAGAGATTTGGAAAGGTTTCTTAGTAAATAATCTCAGGCTCTGAT 256
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DB 429 AGGGAGAGATTTGTACACGCTTATCCAAAGAGATGATGTACAGAGAAGATGTC 488
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DB 489 AAATTCCTACCTGGTGAAGCTGCTACCTGTTAAGCACTACT-AGCCTGGGAATATTT 547
OY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThr 224
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DB 965 TAGACTGCAATAACTGTATAGAGA-GAAATTCATCCCGCATTTAAACCTGCACAGCGCA 1023
OY 364 erGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerP 384
DB 1024 GGCCCTGAAGATATCTTATTTTGAATCTGATTCACAAACCTCCCAAGATTCAC 1083
OY 384 roAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrVal 404

DB 1084 CT---GGCATTCACCTAGTGTAAATGCATCAGCTTTTGGGGGTTAGTTTGTG 1140
OY 404 la 404
DB 1141 CT 1142

Search completed: November 18, 2002, 12:17:57
Job time : 95 secs

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 20:55:41 ; Search time 2846 Seconds

(without alignments)
5061.802 Million cell updates/sec

Title: US-09-762-258-2
Perfect score: 2614
Sequence: 1 MARGRRARAGAAVAFLD.....PIRPPSGTKSKRGGRGR 495

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-UNITS-bits -START=1 -END=1 -MATRIX-D1osum62 -TRANS-human40.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2605	99.7	1720	9 AF099739	AF099739 Homo sapi
3	2600	99.5	1807	9 BC000094	BC000094 Homo sapi
4	2594	99.2	1716	9 AF076931	AF076931 Homo sapi
5	2594	99.2	1732	6 AR206888	AR206888 Sequence
6	2586	98.9	1788	9 BC006106	BC006106 Homo sapi
7	2572.5	98.4	1744	9 AB019245	AB019245 Homo sapi
8	2364.5	90.5	1491	10 MM07938	AJ007938 Mus muscu
9	1749	66.9	1778	4 OCG3PK	X54415 Rabbitt mRna
10	1748	66.9	2346	6 AX333655	AX333655 Sequence
11	1748	66.9	2346	9 H0MP70S6KA	M60724 Human p70 r
12	1746	66.8	1800	10 RAT56KIN3	M57428 Rat S6 Kina
13	1745	66.8	1791	9 H0MP70S6KB	M60725 Human p70 r
14	1740	66.6	2287	10 RAT56PK	M58340 Rat S6 prot
15	1692.5	64.7	1717	5 XLA131521	AJ131521 Xenopus la
16	1468	56.2	1775	3 AF282407	AF282407 Artemia f
17	1455	55.7	2556	6 A69489	A69489 Sequence 1
18	1455	55.7	2556	6 A72166	A72166 Sequence 1
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20	1447	55.4	2481	3 DMU67304	U67304 Drosophila
21	1415	54.1	3479	3 AY095090	AY095090 Drosophila
22	1385.5	53.0	1607	6 AR086879	AR086879 Sequence
23	1383	52.9	168567	9 AF003419	AF003419 Homo sapi
24	1383	52.9	169144	2 AC005849	AC005849 Homo sapi
25	1340	51.3	135116	2 AP002437	AP002437 Homo sapi
26	1271.5	48.6	269355	2 AC109138	AC109138 Mus muscu
27	1266.5	48.5	2770	3 AF294915	AF294915 Aplysia c
28	1211.5	46.3	843	6 AX250156	AX250156 Sequence
29	1149	46.0	54667	2 AC014816	AC014816 Drosophila
30	1149	44.0	173386	3 AC010716	AC010716 Drosophila
31	1149	44.0	173558	3 AC093500	AC093500 Drosophila
32	1149	44.0	286583	3 AE003565	AE003565 Drosophila
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36	980.5	37.5	3206	9 BC014966	BC014966 Homo sapi
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39	966	37.0	3061	6 H0MS6KINA	AX409499 Sequence
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42	961.5	36.8	5240	10 MM0131021	AJ131021 Mus muscu
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RESULT 1

ALIGNMENTS

LOCUS	ABO16869		1735 bp	mRNA	linear	PRI 13-NOV-1998
DEFINITION	Homo sapiens mRNA for p70 ribosomal S6 kinase beta, complete cds.					
ACCESSION	ABO16869					
VERSION	ABO16869.1	GI:3882084				
KEYWORDS	p70 ribosomal S6 kinase beta.					
SOURCE	Homo sapiens human embryonic kidney cell_line:HEK293	cDNA to mRNA.				
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	Gout,I., Maumel,T., Hara,K., Tsujishita,Y., Filonenko,V., Materfield,M.D. and Yonezawa,K.					
TITLE	Molecular cloning and characterization of a novel p70 S6 kinase, p70 S6 kinase beta containing a proline-rich region					
JOURNAL	J. Biol. Chem. 273 (46), 30061-30064 (1998)					
REFERENCE	2 (bases 1 to 1735)					
AUTHORS	Yonezawa,K., Gout,I. and Hara,K.					
TITLE	Direct Submission					
JOURNAL	Submitted (12-AUG-1998) Kazuyoshi Yonezawa, Kobe University, Biosignal Research Center; I-I, Rokkodai-cho, Nada-ku, Kobe, 657-8501, Japan (E-mail:yonezawa@bioinf.kobe-u.ac.jp, Tel.:81-78-803-1250, Fax:81-78-803-1259)					
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Percent Similarity:	100.00%	Conservative:	0			
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VERSION AF099739.1 GI:4454856
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ORGANISM Homo sapiens.
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AUTHORS Koh,H., Jee,K., Lee,B., Kim,J., Kim,D., Yun,Y.H., Kim,J.W.,
Choi,H.S. and Chung,J.
TITLE Cloning and characterization of a nuclear S6 kinase, S6
JOURNAL kinase-related kinase (SRK); a novel nuclear target of Akt
MEDLINE 99422046
PUBMED 10490848
REFERENCE 2 (bases 1 to 1720)
AUTHORS Koh,H.J., Lee,B.N., Choi,H.S. and Chung,J.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1998) Biological sciences, Korea Institute of
Advanced Science and Technology, Kusong, Yusong, Taejon 305-701,
South Korea
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Oy	383	SerProAaspSerThAlaIleuSerGusSerAlaAngInAlaPheLeuGlyPheThrTyr	Oy	403	ValAlaProSerValIleuAspSerIleLeuGlyGlyPheSerPheGlnProIlySerIleuArg	Oy	423	SerProAlaArgIleuAsnSerSerProAlaValAlProValSerProLeuLysPheSerPro	Oy	443	PheGluGlyPheArgProSerProSerLeuProGluAlProThGluIleuProleuProPro	Db	1327	TTTGAGGGGTTTCGGGCCCGACGCCCGCTCGGAGGCCACCGAGACTTACTCTCA	Db	1387	CTCCGTGCACACCGCCCGCCCTCGACACACCGCCCTCTCCATCCGTCGCCCGCCACGAGG	Oy	483	ThrIlySerSerLysArgGlyArgGlyArgProGlyArg	Db	1447	ACCAAGAGTCCACAGAGGGCGCTGGCGCTCCAGGCGC	RESULT 3	BC000094	BC000094	LOCUS	BC000094	1807 bp	mRNA	linear	PRI 12-JUL-2001	Homio sapiens, ribosomal protein S6 kinase, 70kD, polypeptide 2,	clone MGC:1848 IMAGE:3508140, mRNA, complete cds.	BC000094	BC000094	1	GI:12652690	MGC.	Homio sapiens.	Homio sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 1807)	Strausberg, R.	Direct Submission	Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.ncl.nih.gov	Contact: MGC help desk	Email: cgapbs-remail.nih.gov	Tissue Procurement: ATCC	cDNA Library Preparation: Rubin Laboratory	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	DNA Sequencing by: Institute for Systems Biology	http://www.systemsbio.org	contact: amadan@systemsbio.org	Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	Series: IRAL Plate: 7 Row: h Column: 4	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4165310.	Location/Qualifiers	1. 1807	/organism="Homio sapiens"	/db_xref="locusID:6199"	/db_xref="taxon:9606"	/clone="MGC:1848 IMAGE:3508140"	/issue_type="Brain, neuroblastoma"	/clone_id="NIH MGC_19"	/lab_host="DH10B-R"	/note="vector: pOTB7"	/codon_start=1	65..1513

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QY	Db	Accession	Version	KeyWords	Organism	LOCUS	DEFINITION	REFERENCE	AUTHORS
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Db 755	GCGACCAATTGAGTACATGGCCCTGAGATTCTGGTGGCCAGTGGCCACAAACCGGGCTGTG	814							
QY 264	AspItrPserLeuGIAlAleuMetYrAspMetIleuThrGIYserProProPheThr	283							
Db 815	GACTGTGTGACCTGTGGGGCCCTGATTGACACATGCTCATTGATGTCCCGCCCTTTTACC	874							
QY 284	AlaGIuAsnArgIYsIYsThrMetAspIYsIleIleArgIYIYsLeuAlaLeuProPro	303							
Db 875	GCAGAGAACCGGAGAAACCATGATGAATCATCATCAGGGGCAAGCTGGACCTGCCCCC	934							
QY 304	TyrLeuThrProAspAlaArgAspLeuValIYsIYsPheLeuIYsArgAsnProSerGIu	323							
Db 935	TACCTCACCCAGATGAGCCCGGGACCTTGTCAAAAAGTTTCTGAACCGGAATCCACGCAG	994							
QY 324	ArgIleGIYGIYGIYProGIYAspAlaAlaAspValGIuATGnIAsPProPhePheArgIis	343							
Db 995	CGGATTTGGGGGTGGGCCACAGGGGATCTCTCTGATGTGCAGAGACATCCCTTTTTCGGGAC	1054							
QY 344	MetAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGIu	363							
Db 1055	ATGATTTGGAGACGACTTCTGGCTGGCTGGGTGGACCCCTTTCAGGCTCTGTCTGCAG	1114							
QY 364	SerGIuGIuAspValSerGIuPheAspThrArgPheThrArgGIuInThrProValAspSer	383							
Db 1115	TCAGGGAGAGAGTGAGCCAGTTGATATCCGCTTCACAGGCAACGCCGGTGGACAGT	1174							
QY 384	ProAspAspThrAlaIleuSerGIuSerGIuSerGIuAlaSerGIuAlaPheLeuGIYIYsPheThrYrAl	403							
Db 1175	CCTGATGACACAGCCCTCAGAGGAGTGCCCAACGAGCTTCTGTGGCTTCACATAGCTG	1234							
QY 404	AlaProSerValIleuAspSerIleYsGIuGIYIYsPheSerPheGIuProIYsLeuArgSer	423							
Db 1235	GCGCGCTGTGCTGGAGAGATCATCAAGAGAGGAGCTTCTTTCACACCCAGCTGGGCTCA	1294							
QY 424	ProArgArgLeuAsnSerSerProArgAlProValSerProLeuIYsPheSerProPhe	443							
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QY 444	GIuGIYIYsPheArgProSerProSerLeuProGIuProThrGIuLeuProLeuProLeu	463							
Db 1355	GAGGGGTTCGGCCAGCCCGACCTGCGGAGGCCACGAGCTACCTGCTCACTC	1414							
QY 464	LeuProProProProProProSerThrThrAlaProLeuProIleArgProProSerGIYThr	483							
Db 1415	CTGCGACCGCGCGCCCTGCACACCGCCCTCTGCCCATCTGCCCTTCAGAGGAC	1474							
QY 484	IYsIYsSerIYsArgGIYArgGIYArgProGIYArg	495							
Db 1475	AAGAAGTCCAGAGGGGCGCTGGCGCTCAGGGCGC	1510							
RESULT 4									
LOCUS	AF076931	1716 bp	mRNA	linear	PRI 24-NOV-2000				
DEFINITION	Homo sapiens serine/threonine kinase 14 beta (SKI4B) mRNA,								
ACCESSION	AF076931								
VERSION	AF076931.1								
KEYWORDS									
SOURCE	Homo sapiens.								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 1716)								
AUTHORS	Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.								
JOURNAL	Characterization of SKI2, a novel kinase homologous to SKI1								
MEDLINE	Oncogene 18 (36), 5108-5114 (1999)								
PUBMED	10490847								
REFERENCE	2 (bases 1 to 1716)								
AUTHORS	Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.								

[illegible]

QY 165 SerGlyGlyGluLeuPheThrHisLeuGluValArgGlyGlyIlePheLeuGluAspThrAla 184
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 QY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIle 204
 DB 549 TGGCTTACCTGGCTAGATTCACGCTGGCCCTGGCCATCTCCACATCCAGGGCATCATC 608
 QY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThr 224
 DB 609 TACCGGAGCTCAAGCCCGAGAACATCATGCTCAGCAGCGAGCGCCACATCAACATGAC 668
 QY 225 AspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGly 244
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 DB 789 TGGTGGAGCGCTGGGGCCCTGATGTCAGCATGCTCAGTGGATCGCGCCCTTTACCGCA 848
 QY 285 GluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyr 304
 DB 849 GAGAACCGGAGAAACCAATGATATCATCATCAGGGGCAAGCTGGCAGCTGCCCTCAG 908
 QY 305 LeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArg 324
 DB 909 CTCACCCCAAGATGCCCGGAGCCTTGTCAAAAATTTCTGAACGGAGATCCACCGAGCG 968
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 QY 385 AspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAla 404
 DB 1149 GATGACACAGCCCTGACGAGAGTGGCAACACAGCCTTCTCGGGCTTCACATTCGTGG 1208
 QY 405 ProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerPro 424
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 DEFINITION Sequence 1 from patent US 6372467.

ACCESSION AR206888
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1732)
 AUTHORS Blenis,J., Lee-Fruman,K.K. and Kuo,C.J.
 TITLE p546k and p856k genes, proteins, primers, probes, and detection methods
 JOURNAL Patent: US 6372467-A 1 16-APR-2002;
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 source Location/Qualifiers
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 DEFINITION BC006106.1 GI:13543927
 ACCESSION
 VERSION
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1788)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
 Email: gcaps-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLN)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Kan Guln,
 Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Zutra.

Clone distribution: MGC clone distribution information can be found
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 Series: IRL Plate: 18 Row: a Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Genomescan gene
 prediction.

FEATURES

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CDS

BASE COUNT 401 a 539 c 535 g 313 t
 ORIGIN

Alignment Scores:

Score: 4.17e-133 Length: 1788
 Pred. No.: 2586.00 Matches: 490
 Percent Similarity: 99.59% Conservatve: 0
 Best Local Similarity: 99.59% Mismatches: 2
 Query Match: 98.93% Indels: 0
 DB: 9 Gaps: 0

US-09-762-258-2 (1-495) x BC006106 (1-1788)

Oy 4 GylrArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGlu 23
 Db 9 GGCGCAGCGGGCGGGGGCGGGCGCCGCAATGCGGGCGCTTGTGATTGGATTGGAG 68
 Oy 24 ThrGluGluGlySerGlyGlyGlyGlyGluGluProGluLeuSerProAlaAspAlaCysPro 43
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 Db 1449 AAGAACTCCAAAGAGGGGCGCTGGGCTCCAGGGCCG 1484

RESULT 7
 AB019245 1744 bp mRNA linear PRI 06-FEB-1999
 LOCUS Homo sapiens p70 S6Kb mRNA for s6 kinase b, complete cds.
 DEFINITION
 ACCESSION AB019245.1 GI:4165310
 VERSION AB019245.1
 KEYWORDS p70 S6Kb; s6 kinase b.
 SOURCE Homo sapiens cell_line:erythrocyte leukemia cell CDNA to mRNA.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Salton,M., ten Dijke,P., Miyazono,K. and Ichijo,H.
 TITLE Cloning and characterization of p70(S6K beta) defines a novel family of p70 S6 kinases
 JOURNAL Biochem. Biophys. Res. Commun. 253 (2), 470-476 (1998)
 MEDLINE 99097259
 JOURNAL 2 (bases 1 to 1744)
 AUTHORS Salton,M. and Ichijo,H.
 TITLE Direct Submission
 JOURNAL Submitted (27-OCT-1998) Masao Salton, Tokyo Medical and Dental Univ., Dept. of Biomaterials Science, Faculty of Dentistry, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8549, Japan (E-mail:msalton-indemuln.ac.jp, Tel:+81-3-5803-5473, Fax:+81-3-5803-0192)

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 Query Match: 98.41%
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US-09-762-258-2 (1-495) x AB019245 (1-1744)
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[illegible]

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Db	1160	CCTGATGACACAGCCCTCAGGAGAGGTCCAACACAGCCCTTCCTGGGCTTCACATAGCTG	1219
OY	404	AlaProSerValIleuAspSerIlelySgluclyPheSerPheGlnProlysLeuArgSer	423
Db	1220	GGCGGCTCTGTCCTGGACAGCATCAAGAGGAGGCTTCTCTTCACGCCAACCTGGCTCA	1279
OY	424	ProArGArgLeuAnSerSerProArgAlaProValSerProLeuLysPheSerProPhe	443
Db	1280	CCACAGGCGCCCTCAACAGTAGCCCGCGGGCCCGCCGACACCCCTCAAGTCTCCCTTTT	1339
OY	444	GluclyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu	463
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OY	464	LeuProProProProProSerThrThraAlaProLeuProIleArgProProSerGlyThr	483
Db	1400	CTGGCACCGCGCGCCCTCGACACCCCGCTCTCCCATCCGTCGCCCTCAGGGACC	1459
OY	484	LysLysSerLysArgGlyArgGlyArgProGlyArg	495
Db	1460	AAGAAGTCCAAAGAGGGCGGTGGGCTCCACAGGCGC	1495
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VERSION	AJ007938.1		
KEYWORDS	S6 kinase 2; S6K2 gene.		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1491)		
TITLE	Kozma, S.C.		
JOURNAL	Direct Submission		
REMARK	Submitted (15-JUL-1998) Kozma S.C., Growth Control, Friedrich		
REFERENCE	Miescher Institute, P.O.Box 2543, Basel, CH-4002, SWITZERLAND		
AUTHORS	revised by author		
TITLE	2 (bases 1 to 1491)		
JOURNAL	Shima, H., Pende, M., Chen, Y., Fumagalli, S., Thomas, G. and Kozma, S.C.		
MEDLINE	Disruption of the p70(s6k)/p55(s6k) gene reveals a small mouse		
PUBMED	phenotype and a new functional S6 kinase		
FEATURES	EMBO J. 17 (22), 6649-6659 (1998)		
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ORIGIN

Alignment Scores:

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 Score: 2364.50 Matches: 449
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US-09-762-258-2 (1-495) x MMU7938 (1-1491)

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 QY 74 ArgIleGlyProHisCysPheGluLeuLeuArgValaLeuGlyLysGlyLysGlyLys 93
 Db 181 CCATCTGGGCCCCACGCTTTGAGCTAGTACTGCGGCAAGGGGGGCTATGGCAAG 240
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RESULT 9
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 DERIVATION protein S6 kinase.

ACCESSION X54415
 VERSION X54415.1 GI:1561
 KEYWORDS protein kinase; serine threonine kinase.
 SOURCE Oryctolagus cuniculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 1778)
 AUTHORS Killmann,M.W.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-1990) Killmann M.W., Institut fuer Physiologische
 Chemie, Universitaet Bochum, Postfach 10 21 48, D-4630 Bochum 1,
 FRG

REFERENCE 2 (bases 1 to 1778)
 AUTHORS Harman,B. and Killmann,M.W.
 TITLE cdna encoding a 59 kDa homolog of ribosomal protein S6 kinase from
 rabbit liver
 JOURNAL FEBS Lett. 273 (1-2), 248-252 (1990)
 MEDLINE 91032193
 PUBMED 1699810

FEATURES
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DEFINITION Sequence 4164 from Patent WO0194629.
ACCESSION AX333655
VERSION AX333655.1 GI:18124374
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
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TITLE
 Cancer gene determination and therapeutic screening using signature
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 JOURNAL
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 Avallon Pharmaceuticals (US)
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 QY 464 LeuProProProProProSer-----Thr 471
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 QY 484 ----- 484
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 DEFINITION
 M60724
 VERSION M60724.1 GI:189507
 KEYWORDS p70 ribosomal S6 kinase alpha-1.
 SOURCE Human liver hepatoma, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2346)

AUTHORS Grove, J.R., Banerjee, P., Balasubramanyam, A., Coffier, P.J.,
 Price, D.J., Avrich, J. and Woodgett, J.R.
 TITLE Cloning and expression of two human p70 S6 kinase polypeptides
 differing only at their amino termini
 JOURNAL Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
 MEDLINE 92017834
 PUBMED 1922062

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BASE COUNT 750 a 453 c 558 g 585 t

ALIGNMENT SCORES:
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 Best Local Similarity: 64.36% Mismatches: 80
 Query Match: 66.87% Indels: 66
 Gaps: 8

US-09-762-258-2 (1-495) x HUMPT056KA (1-2346)

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 Db 88 GCTGAGGACATGGCGAGAGTGTTCACATAGACCTGGACACCCAGAGAGACCGGGCTCT 147
 QY 31 GluglygluProgluLeuSerProAlaaspAlaCysProLeuAlaGlu---LeuArghla 49
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 QY 472 ThrAlaProLeuProIleArgProProSerGlyThrHis----- 484
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DEFINITION Rat S6 kinase mRNA, complete cds.
ACCESSION M57428 M35864
VERSION M57428.1 GI:206839
KEYWORDS S6 kinase.
SOURCE Rat (Strain Sprague-Dawley) liver, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1800)
AUTHORS Kozma,S.C., Ferraril,S., Basand,P., Siegmann,M., Totty,N. and Thomas,G.
TITLE Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of the second messenger subfamily
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7365-7369 (1990)
MEDLINE 91017506
PUBMED 1699226
REFERENCE 2 (sites)
AUTHORS Lane,H.A., Morley,S.J., Doree,M., Kozma,S.C. and Thomas,G.
TITLE Identification and early activation of a Xenopus laevis p70s6k following progesterone-induced meiotic maturation
JOURNAL EMBO J. 11 (5), 1743-1749 (1992)
MEDLINE 92258384
PUBMED 1374712
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BASE COUNT 556 a 355 c 464 g 425 t
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ACCESSION M60725.1 GI:1895109
VERSION p70 ribosomal S6 kinase alpha-II.
KEYWORDS p70 ribosomal S6 kinase alpha-II.
SOURCE Human liver hepatoma, CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1791)
Grove,J.R., Banerjee,P., Balasubramanyam,A., Coffey,P.J.,
Price,D.J., Avruch,J. and Woodgett,J.R.
TITLE Cloning and expression of two human p70 S6 kinase polypeptides
differing only at their amino termini
JOURNAL Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
MEDLINE 92017834
PUBMED 1922062

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Query Match: 66.76% Indels: 56
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US-09-762-258-2 (1-495) x HUMP70S6KB (1-1791)
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Db 1047 CCTGGGAGACGTGAGAAAGTCAAGCTCATTCATCTTATGACACATTAATCTGGGAAGA 1106

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LOCUS 2287 bp mRNA linear ROD 27-APR-1993
DEFINITION Rat S6 protein kinase mRNA, complete cds.
ACCESSION M58340.1 GI:206841
VERSION M58340.1 GI:206841
KEYWORDS S6 protein kinase; Insulin/mitogen stimulated protein kinase; p70
SOURCE Rat, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Banerjee,P., Ahmed,M.F., Grove,J.R., Kozlosky,C., Price,D.J. and
Avruch,J.
TITLE Molecular structure of a major insulin/mitogen-activated 70-kDa S6
protein kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8550-8554 (1990)
MEDLINE 91046033
PubMed 2236064
FEATURES
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US-09-762-258-2 (1-495) x RAT56PK (1-2287)
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 VERSION A1131521.1
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Xenopodinae; Xenopus.
 Schaub, M.S., Kim, S.H., Terada, N., Edfjall, C., Kozma, S.C., Thomas, G.
 and Maller, J.L.
 p70(S6K) controls selective mRNA translation during oocyte
 maturation and early embryogenesis in Xenopus laevis
 JOURNAL Mol. Cell. Biol. 19 (4), 2485-2494 (1999)
 MEDLINE 99182435
 PUBMED 10082514

REFERENCE 2 (bases 1 to 1717)
 AUTHORS Kozma, S.C.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1998) Kozma S.C., Growth Control, Friedrich
 Miescher Institute, P.O. Box 2543 Basel, CH-4002, SWITZERLAND
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 QY 43 ProLeuAlaGluLeuArg-----AlaAlaGlyLeuGluProVal 55
 DB 172 ACCTTTATGTAGTTCATGACGACCATGGAGTATCTTATGACATGACATGAG----- 225
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 QY 136 LeuGluSerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyCly 155
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